STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number 160235

TO: Sumesh Kaushal
Location: REM-2B85/2C70
Art Unit: 1636
Monday, April 11, 2005

Case Serial Number: 09/925674

From: Deirdre Arnold
Location: Biotech-Chem Library
REM 1A64
Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

Search Notes

RUSH

Please feel free to contact me if you have any questions or would like to amend the search.

Thank you for using STIC services.

Regards,
Deirdre Arnold

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 14:45:43 ; Search time 3068.26 Seconds
(without alignments)
9206.966 Million cell updates/sec

Title: US-09-925-674B-6
Perfect score: 583
Sequence: 1 atggcgaccccagcctcggc.....ctttttttgctagcaagtgaa 583

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	583	100.0	583	6	AX022529	AX022529 Sequence
2	583	100.0	583	6	AX030817	AX030817 Sequence
3	577.2	99.0	582	6	AX481423	AX481423 Sequence
4	577.2	99.0	582	9	HSU59747	U59747 Human Bcl-w
5	575	98.6	3542	9	D87461	D87461 Homo sapien
6	572.4	98.2	582	6	CQ730429	CQ730429 Sequence
7	567.8	97.4	579	6	AR020780	AR020780 Sequence
8	527.6	90.5	582	10	AF096291	AF096291 Rattus no
9	527.6	90.5	1110	10	AY185100	AY185100 Rattus no
10	527.6	90.5	3487	10	AY185098	AY185098 Rattus no
11	527.6	90.5	3545	10	BC074021	BC074021 Rattus no
12	523	89.7	579	6	AR020779	AR020779 Sequence
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15	511.8	87.8	3442	10	AK172925	AK172925 Mus muscu
16	510	87.5	3473	10	AY170344	AY170344 Mus muscu
17	501	85.9	581	6	AX022531	AX022531 Sequence
18	501	85.9	581	6	AX030819	AX030819 Sequence
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20	441.2	75.7	223933	2	AC097389	AC097389 Rattus no
21	424	72.7	1098	6	AR432565	AR432565 Sequence
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26	383.8	65.8	148278	2	AC079885	AC079885 Rattus no
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43	150	25.7	150	6	CQ179440	CQ179440 Sequence
44	150	25.7	150	6	CQ203800	CQ203800 Sequence
45	150	25.7	150	6	CQ227167	CQ227167 Sequence

ALIGNMENTS

RESULT 1
AX022529
LOCUS AX022529 583 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 6 from Patent EP0932674.
ACCESSION AX022529
VERSION AX022529.1 GI:10046125
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes
JOURNAL Patent: EP 0932674-A 6 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
FEATURES Location/Qualifiers
source 1. .583
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
CDS 1. .583
/note="unnamed protein product"
/codon_start=1
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/translation="MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
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ORIGN

Query Match 100.0%; Score 583; DB 6; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.5e-121;
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

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Db       361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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RESULT 2
AX030817
LOCUS AX030817 583 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 6 from Patent WO9735971.
ACCESSION AX030817
VERSION AX030817.1 GI:10278311
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes
JOURNAL Patent: WO 9735971-A 6 02-OCT-1997;
ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU) ; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)

FEATURES Location/Qualifiers
source 1. .583
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
CDS 1. .583
/note="unnamed protein product"
/codon_start=1
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/db_xref="GI:10278312"
/translation="MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
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ORIGIN

Query Match 100.0%; Score 583; DB 6; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.5e-121;
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Qy        61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Qy       121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Qy       481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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RESULT 3
AX481423
LOCUS AX481423 582 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 37 from Patent WO02055693.
ACCESSION AX481423
VERSION AX481423.1 GI:22316337
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kreutzer,R., Limmer,S., Rost,S. and Hadwiger,P.
TITLE Method for inhibiting the expression of a target gene
JOURNAL Patent: WO 02055693-A 37 18-JUL-2002;
Ribopharma AG (DE)

FEATURES Location/Qualifiers
source 1. .582
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 99.0%; Score 577.2; DB 6; Length 582;
Best Local Similarity 99.5%; Pred. No. 7.2e-120;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy         1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Qy        61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Db        61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Qy       181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db       481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
Qy       541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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RESULT 4
HSU59747
LOCUS       HSU59747                582 bp    mRNA    linear   PRI 29-SEP-1996
DEFINITION  Human Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION   U59747
VERSION     U59747.1  GI:1572492
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G.,
            Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
  TITLE     bcl-w, a novel member of the bcl-2 family, promotes cell survival
  JOURNAL   Oncogene 13 (4), 665-675 (1996)
  MEDLINE   96358615
   PUBMED   8761287
REFERENCE   2  (bases 1 to 582)
  AUTHORS   Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and
            Cory,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
            Eliza Hall Institute of Medical Research, PO Royal Melbourne
            Hospital, Parkville, Victoria 3050, Australia
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ORIGIN

  Query Match           99.0%;  Score 577.2;  DB 9;  Length 582;
  Best Local Similarity 99.5%;  Pred. No. 7.2e-120;
  Matches  579;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Qy        61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
Db        61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
Qy       121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
Db       121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
Qy       181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db       301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Qy       541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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RESULT 5
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LOCUS       D87461                  3542 bp    mRNA    linear   PRI 10-JAN-2004
DEFINITION  Homo sapiens mRNA for KIAA0271 gene, partial cds.
ACCESSION   D87461
VERSION     D87461.1  GI:1944417
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y.,
            Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.
  TITLE     Prediction of the coding sequences of unidentified human genes. VI.
            The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
            analysis of cDNA clones from cell line KG-1 and brain
  JOURNAL   DNA Res. 3 (5), 321-329 (1996)
  MEDLINE   97191544
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   PUBMED     9039502
REFERENCE     2  (bases 1 to 3542)
  AUTHORS     Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
  TITLE       Direct Submission
  JOURNAL     Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute;
              1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
              (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
FEATURES             Location/Qualifiers
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                     /clone="HA6752"
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                     /protein_id="BAA19666.2"
                     /db_xref="GI:40788933"
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ORIGIN

  Query Match             98.6%;  Score 575;  DB 9;  Length 3542;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-119;
  Matches  578;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

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Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        357 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 416

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 476

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Db        477 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 536

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        537 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 596

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Db        597 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 656

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 716

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 583
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Db        717 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 759


RESULT 6
CQ730429
LOCUS       CQ730429                582 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 16363 from Patent WO02068579.
ACCESSION   CQ730429
VERSION     CQ730429.1  GI:42304244
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 16363 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .582
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             98.2%;  Score 572.4;  DB 6;  Length 582;
  Best Local Similarity   99.0%;  Pred. No. 8.8e-119;
  Matches  576;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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RESULT 7
AR020780
LOCUS       AR020780                 579 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 2 from patent US 5789201.
ACCESSION   AR020780
VERSION     AR020780.1  GI:3975395
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 579)
  AUTHORS   Guastella,J.
  TITLE     Genes coding for bcl-y a bcl-2 homologue
  JOURNAL   Patent: US 5789201-A 2 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .579
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             97.4%;  Score 567.8;  DB 6;  Length 579;
  Best Local Similarity   98.8%;  Pred. No. 9.6e-118;
  Matches  572;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Db        121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
              |||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579


RESULT 8
AF096291
LOCUS       AF096291                 582 bp    mRNA    linear   ROD 28-FEB-2000
DEFINITION  Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION   AF096291
VERSION     AF096291.1  GI:3747129
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Hamner,S., Skoglosa,Y. and Lindholm,D.
  TITLE     Differential expression of bcl-w and bcl-x messenger RNA in the
            developing and adult rat nervous system
  JOURNAL   Neuroscience 91 (2), 673-684 (1999)
  MEDLINE   99292146
   PUBMED   10366024
REFERENCE   2  (bases 1 to 582)
  AUTHORS   Hamner,S., Skoglosa,Y. and Lindholm,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
            University, Box 587, BMC, Uppsala 751 23, Sweden
FEATURES             Location/Qualifiers
     source          1. .582
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /tissue_type="brain"
                     /dev_stage="postnatal"
     gene            1. .582
                     /gene="bcl-w"
     CDS             1. .582
                     /gene="bcl-w"
                     /note="Bcl-2 family member"
                     /codon_start=1
                     /product="Bcl-w"
                     /protein_id="AAC64200.1"
                     /db_xref="GI:3747130"
                     /translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
                     AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
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                     RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
ORIGIN

  Query Match             90.5%;  Score 527.6;  DB 10;  Length 582;
  Best Local Similarity   94.2%;  Pred. No. 1.1e-108;
  Matches  548;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              |||||||||||||||||||||||||||||||||||||||||||||| ||||| |||||||| |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              |||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              ||||| |||||||||||||| ||||||||||||||||||||||| ||||| || |||||||
Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Db        361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420
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Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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RESULT 9
AY185100
LOCUS AY185100 1110 bp mRNA linear ROD 24-JUN-2003
DEFINITION Rattus norvegicus BCL-WEL mRNA, complete cds.
ACCESSION AY185100
VERSION AY185100.1 GI:32185284
KEYWORDS .
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1110)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Bcl-2-related protein family gene expression during oligodendroglial differentiation
JOURNAL J. Neurochem. 85 (6), 1500-1512 (2003)
MEDLINE 22672518
PUBMED 12787069
REFERENCE 2 (bases 1 to 1110)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Neurology Research, The Children's Hospital of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center Blvd., Philadelphia, PA 19104, USA
FEATURES Location/Qualifiers
source 1. .1110
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/strain="Sprague-Dawley"
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CDS 431. .1090
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/db_xref="GI:32185285"
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ORIGIN

Query Match 90.5%; Score 527.6; DB 10; Length 1110;
Best Local Similarity 94.2%; Pred. No. 1e-108;
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Db        509 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 568

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Db        569 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 628

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Db        629 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 688

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||||  |||||  ||||||||  ||  ||||||||||||||||||||||||||||||
Db        689 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 748

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||  ||||||||||||||  ||||||||||||||||||||||||||  |||||  ||  ||||||
Db        749 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 808

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||||  ||||||||||||||||||||||  ||  |||||  |||  ||||||||
Db        809 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 868

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              ||||||||||  |||||||||  ||||||||||||  ||  |||  ||||||||||||||||
Db        869 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 928

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Db        929 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 988

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Db        989 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 1048

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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Db       1049 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 1090
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RESULT 10
AY185098
LOCUS AY185098 3487 bp mRNA linear ROD 24-JUN-2003
DEFINITION Rattus norvegicus BCL-W mRNA, complete cds.
ACCESSION AY185098
VERSION AY185098.1 GI:32185280
KEYWORDS .
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 3487)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Bcl-2-related protein family gene expression during oligodendroglial differentiation
JOURNAL J. Neurochem. 85 (6), 1500-1512 (2003)
MEDLINE 22672518
PUBMED 12787069
REFERENCE 2 (bases 1 to 3487)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Neurology Research, The Children's Hospital of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center Blvd., Philadelphia, PA 19104, USA
FEATURES Location/Qualifiers
source 1. .3487
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/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
CDS 170. .751
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/product="BCL-W"
/protein_id="AAO64468.1"
/db_xref="GI:32185281"
/translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF GAALCAESVNKEMEPLVGQVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEAR RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
ORIGIN

Query Match 90.5%; Score 527.6; DB 10; Length 3487;
Best Local Similarity 94.2%; Pred. No. 9.1e-109;
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Db        230 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 289

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Db        290 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 349

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        350 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 409

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Db        410 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 469

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              |||||||||||| |||||||||||||||||||||| || ||||| ||| ||||||||
Db        470 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 529

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||| ||||||||| |||||||||||||| || ||| ||||||||||||||||
Db        530 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 589

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        590 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 649

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        650 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 709

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
              |||||||||||||||||||||||||||||||||||||||||
Db        710 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 751
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RESULT 11
BC074021
LOCUS BC074021 3545 bp mRNA linear ROD 30-JUN-2004
DEFINITION Rattus norvegicus cDNA clone MGC:91704 IMAGE:7105621, complete cds.
ACCESSION BC074021
VERSION BC074021.1 GI:49256646
KEYWORDS MGC.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 3545)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 3545)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (23-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 175 Row: p Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11177885.

FEATURES Location/Qualifiers
source 1. .3545
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="MGC:91704 IMAGE:7105621"
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/lab_host="DH10B"
/note="Vector: pExpress1"
CDS 199. .780
/codon_start=1
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/translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
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RLREGNWASVRTVLTGAVALGALVTVGAFFASK"

ORIGIN

Query Match 90.5%; Score 527.6; DB 10; Length 3545;
Best Local Similarity 94.2%; Pred. No. 9e-109;
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              |||||||||||||||||  |||||||||||||||||||| ||||| |||||||||||| |||
Db        199 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 258

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              |||||||||||||||||||||||||||||||||||| ||||| |||||||||||| |||
Db        259 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 318

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Db        319 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 378
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Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        379 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 438

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
Db        439 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 498

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
Db        559 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 618

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
Db        619 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 678

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
Db        679 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 738

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
Db        739 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 780
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RESULT 12
AR020779
LOCUS AR020779 579 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 1 from patent US 5789201.
ACCESSION AR020779
VERSION AR020779.1 GI:3975394
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 579)
AUTHORS Guastella,J.
TITLE Genes coding for bcl-y a bcl-2 homologue
JOURNAL Patent: US 5789201-A 1 04-AUG-1998;
FEATURES Location/Qualifiers
source 1. .579
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 89.7%; Score 523; DB 6; Length 579;
Best Local Similarity 94.0%; Pred. No. 1.2e-107;
Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
Db         61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
Db        361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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RESULT 13
MMU59746
LOCUS MMU59746 582 bp mRNA linear ROD 29-SEP-1996
DEFINITION Mus musculus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION U59746
VERSION U59746.1 GI:1572494
KEYWORDS .
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 582)
AUTHORS Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G., Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
TITLE bcl-w, a novel member of the bcl-2 family, promotes cell survival
JOURNAL Oncogene 13 (4), 665-675 (1996)
MEDLINE 96358615
PUBMED 8761287
REFERENCE 2 (bases 1 to 582)
AUTHORS Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and Cory,S.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
FEATURES Location/Qualifiers
source 1. .582
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/mol_type="mRNA"
/db_xref="taxon:10090"
/chromosome="14"
/cell_line="BaF3"
gene 1. .582
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CDS 1. .582
/gene="bcl-w"
/note="promotes cell survival; Bcl-2 homolog"
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RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
ORIGN

Query Match 89.7%; Score 522.8; DB 10; Length 582;
Best Local Similarity 93.6%; Pred. No. 1.4e-107;
Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Db        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Db        361 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582


RESULT 14
AF030769
LOCUS       AF030769                3476 bp    mRNA    linear   ROD 16-NOV-1997
DEFINITION  Mus musculus BCL-W (Bcl-w) mRNA, complete cds.
ACCESSION   AF030769
VERSION     AF030769.1  GI:2623249
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3476)
  AUTHORS   Ross,A.J., Waymire,K.G., Moss,J.E., Parlow,A.F., Russell,L.D. and
            MacGregor,G.R.
  TITLE     Bcl-w is required for testis homeostasis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3476)
  AUTHORS   Ross,A.J. and MacGregor,G.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1997) Center for Molecular Medicine, Emory
            University, 1462 Clifton Road, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
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                     /gene="Bcl-w"
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     exon            83. .170
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                     /number=2
     exon            171. .610
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     exon            611. .3476
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ORIGIN

  Query Match             89.7%;  Score 522.8;  DB 10;  Length 3476;
  Best Local Similarity   93.6%;  Pred. No. 1.1e-107;
  Matches  545;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Db        179 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 238

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Db        239 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 298

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Db        299 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 358

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        359 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 418

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Db        419 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 478

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Db        479 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 538

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Db        539 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 598

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Db        599 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 658

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Db        659 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 718

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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Db        719 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 760


RESULT 15
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AK172925
LOCUS       AK172925                3442 bp    mRNA    linear   ROD 28-JUL-2004
DEFINITION  Mus musculus mRNA for mKIAA0271 protein.
ACCESSION   AK172925
VERSION     AK172925.1  GI:50510434
KEYWORDS    FLI_CDNA.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Okazaki,N., Kikuno,R.F., Ohara,R., Inamoto,S., Koseki,H.,
            Hiraoka,S., Saga,Y., Seino,S., Nishimura,M., Kaisho,T., Hoshino,K.,
            Kitamura,H., Nagase,T., Ohara,O. and Koga,H.
  TITLE     Prediction of the Coding Sequences of Mouse Homologues of KIAA
            Gene: IV. The Complete Nucleotide Sequences of 500 Mouse
            KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences
            of cDNA Clones Randomly Sampled from Size-Fractionated Libraries
  JOURNAL   DNA Res. 11, 205-218 (2004)
REFERENCE   2  (bases 1 to 3442)
  AUTHORS   Okazaki,N., Kikuno,R.F., Nagase,T., Ohara,O. and Koga,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAY-2004) Hisashi Koga, Kazusa DNA Research
            Institute, Laboratory for Genome Informatics; 2-6-7
            Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)
COMMENT     The CREATE program supported by Japan science and technology
            corporation; cDNA full insert sequencing: Kazusa DNA Research
            Institute; cDNA library construction, clone selection and 5'- &
            3'-end one pass sequencing.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             87.8%;  Score 511.8;  DB 10;  Length 3442;
  Best Local Similarity   93.5%;  Pred. No. 3.3e-105;
  Matches  545;  Conservative    0;  Mismatches   37;  Indels    1;  Gaps    1;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Db          6 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 65

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              |||||||||||||||||||||||||||||||||||| ||||| |||||||| || |||
Db         66 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 125

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              |||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        126 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 185

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db        186 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 245

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Db        426 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 485

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Db        486 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 545

Qy        541 GGGGCCCTGGTAACTGTAGGGGCC-TTTTTTGCTAGCAAGTGA 582
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Search completed: April 10, 2005, 18:37:53
Job time : 3078.26 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 14:40:06 ; Search time 457.785 Seconds
(without alignments)
7538.927 Million cell updates/sec

Title: US-09-925-674B-6
Perfect score: 583
Sequence: 1 atggcgaccccagcctcggc.....ctttttgctagcaagtgaa 583

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	583	100.0	583	2	AAT96577	Aat96577 Human bcl
2	583	100.0	583	2	AAX25134	Aax25134 Human bcl
3	577.2	99.0	582	6	ABV78153	Abv78153 Human bcl
4	577.2	99.0	582	6	ABZ35729	Abz35729 Human bcl
5	577.2	99.0	582	6	ABX09972	Abx09972 Human bcl
6	577.2	99.0	582	6	ABL91694	Abl91694 Human pol
7	575	98.6	3542	8	ABT16642	Abt16642 Human bcl
8	573	98.3	581	2	AAX25132	Aax25132 Human bcl
9	567.8	97.4	579	2	AAV28334	Aav28334 Human bcl
10	567.8	97.4	579	2	AAX15946	Aax15946 cDNA enco
11	527.6	90.5	582	10	ADB52996	Adb52996 Primary r
12	523	89.7	579	2	AAV28333	Aav28333 Rat bcl-y
13	523	89.7	579	2	AAX15945	Aax15945 cDNA enco
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15	501	85.9	581	2	AAT96578	Aat96578 Mouse bcl
16	501	85.9	581	2	AAX25135	Aax25135 Mouse bcl
17	424.8	72.9	1569	13	ACN42800	Acn42800 Human dia
18	424	72.7	1098	2	AAV41925	Aav41925 Nucleotid
19	423.6	72.7	1864	2	AAV59630	Aav59630 Human sec
20	423.6	72.7	1864	6	ABS73617	Abs73617 Human cDN
21	423.6	72.7	1864	9	ACD82760	Acd82760 cDNA sequ
22	423.6	72.7	1864	10	ADI22845	Adi22845 cDNA enco
23	423.6	72.7	1864	12	ADH73847	Adh73847 Human sec
24	423.4	72.6	578	12	ACH77354	Ach77354 Human gen
25	422.4	72.5	433	12	ACH91054	Ach91054 Human gen
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28	152	26.1	590	12	ACH80189	Ach80189 Human gen
29	151	25.9	151	12	ACH93889	Ach93889 Human gen
30	150	25.7	150	4	AAI20236	Aai20236 Probe #10
31	150	25.7	150	4	ABA65269	Aba65269 Human foe
32	150	25.7	150	4	AAI45438	Aai45438 Probe #14
33	150	25.7	150	4	ABA47382	Aba47382 Human bre
34	150	25.7	150	4	ABA32370	Aba32370 Probe #10
35	150	25.7	150	4	AAK39424	Aak39424 Human bon
36	150	25.7	150	4	AAK13683	Aak13683 Human bra
37	150	25.7	150	4	ABS39016	Abs39016 Human liv
38	150	25.7	150	5	AAI05940	Aai05940 Probe #59
39	150	25.7	150	6	ABS13513	Abs13513 Human gen
40	145.2	24.9	660	12	ADH52638	Adh52638 Chinese h
41	144.2	24.7	600	12	ADH52636	Adh52636 Chinese h
42	143	24.5	1742	4	AAF75960	Aaf75960 Rat wild-
43	141.2	24.2	540	12	ADH52634	Adh52634 Chinese h
44	138.2	23.7	702	13	ADQ80676	Adq80676 Rat anti-
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ALIGNMENTS

RESULT 1
AAT96577
ID AAT96577 standard; DNA; 583 BP.
XX
AC AAT96577;
XX
DT 22-APR-1998 (first entry)
XX
DE Human bcl-w DNA.
XX
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .582
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FT /product= "bcl-w"
XX
PN WO9735971-A1.
XX
PD 02-OCT-1997.
XX
PF 27-MAR-1997; 97WO-AU000199.
XX
PR 27-MAR-1996; 96AU-00008965.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Cory S, Adams JM, Gibson LM, Holmgreen SP;
XX
DR WPI; 1997-489635/45.
DR P-PSDB; AAW36047.
XX
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
PT inhibit cell survival, e.g. for treatment of cancer and degenerative
PT diseases.
XX
PS Claim 3; Page 48; 86pp; English.
XX
CC This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
CC family, extracted from an adult brain library. This gene promotes cell

CC survival, so its modulation is useful in treatment of cancer or auto-
CC immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease,
CC myocardial infarct, muscular degeneration, hypoxia, ischaemia, human
CC immunodeficiency virus infection or in cell transplants. Up-regulation of
CC the gene can also be used to modify cell lines cultured in vivo, e.g. to
CC develop new lines, to facilitate isolation of hybridomas and to increase
CC survival of primary explants during genetic modification. It can be used
CC to produce recombinant Bcl-w for therapy, diagnosis, antibody production
CC or screening of potential modulators
XX
SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;

Query Match 100.0%; Score 583; DB 2; Length 583;
Best Local Similarity 100.0%; Pred. No. 1e-135;
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Db        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Db        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 2
AAX25134
ID AAX25134 standard; DNA; 583 BP.
XX
AC AAX25134;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human bcl-w gene derivative.
XX
KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
KW animal model; ss.
XX
OS Homo sapiens.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
DR WPI; 1999-243890/20.
DR P-PSDB; AAY05532.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w.
XX
PS Disclosure; Page 36; 52pp; English.
XX
CC The present sequence is described as a derivative of the human bcl-w gene
CC (see AAX25132) and encodes Bcl-w protein (see AAY05532), a pro-survival
CC member of the Bcl-2 family which is widely expressed and which is
CC essential for spermatogenesis. The invention relates generally to a
CC method of treatment and to an animal model for the identification of
CC molecules and genetic sequences useful for inducing or reducing fertility
CC of male animals. Methods are provided for the treatment of infertility,
CC or for reducing fertility, by modulating spermatogenesis. An animal model
CC carries a mutation is at least one allele of the human or murine bcl-w
CC gene or in a gene associated with bcl-w. Such animals have disorganised
CC seminferous tubules and are substantially infertile, but possess no other
CC major abnormalities as determined by histological examination. They can
CC be used to screen for therapeutic molecules including genetic sequences
CC capable of inducing, enhancing or otherwise facilitating spermatogenesis
CC in animals, or which can induce infertility
XX
SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;

Query Match 100.0%; Score 583; DB 2; Length 583;
Best Local Similarity 100.0%; Pred. No. 1e-135;
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Db        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Db        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 583
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Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 583
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RESULT 3
ABV78153
ID ABV78153 standard; DNA; 582 BP.
XX
AC ABV78153;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human bcl-w DNA SEQ ID NO 37.
XX
KW RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;
KW virucide; protozoacide; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200255693-A2.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2002; 2002WO-EP000152.
XX
PR 09-JAN-2001; 2001DE-01000586.
PR 26-OCT-2001; 2001DE-01055280.
PR 29-NOV-2001; 2001DE-01058411.
PR 07-DEC-2001; 2001DE-01060151.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
DR WPI; 2002-590671/63.
XX
PT Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
PT target and having an overhang.
XX
PS Claim 10; Page 134; 203pp; German.
XX
CC The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in Plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a gene related to the invention
XX
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 99.0%; Score 577.2; DB 6; Length 582;
Best Local Similarity 99.5%; Pred. No. 2.8e-134;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
```

RESULT 4
ABZ35729
ID ABZ35729 standard; DNA; 582 BP.
XX
AC ABZ35729;
XX
DT 07-FEB-2003 (first entry)
XX
DE Human bcl-w polynucleotide SEQ ID NO 37.
XX
KW Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;
KW protozoacide; gene expression; antisense; tumour; infection; Plasmodium;
KW virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
KW Hepatitis C virus; human papilloma virus; gene; ds.
XX
OS Homo sapiens.
XX
PN DE10100588-A1.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2001; 2001DE-01000588.
XX
PR 09-JAN-2001; 2001DE-01000588.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
DR WPI; 2002-683450/74.
XX
PT Inhibiting expression of target genes, useful e.g. for treating tumors,
PT by introducing into cells two double-stranded RNAs that are complementary
PT to the target.
XX
PS Claim 13; Page 30-31; 100pp; German.
XX
CC The invention relates to inhibiting expression of a target gene in a cell
CC by introducing at least two oligoribonucleotides (dsRNAI and II), both

CC with a double-stranded (ds) structure of at most 49 sequential nucleotide
CC pairs. At least part of one strand (S1, S2) of the ds structures in each
CC of dsRNAI and II are complementary to regions in the target gene. The
CC method uses antisense inhibition of gene expression using double stranded
CC RNA inhibition (RNAi). The method is particularly used to treat tumours
CC or infections, especially by Plasmodium or viruses/viroids (pathogenic on
CC humans, animals or plants). The method provides more effective inhibition
CC of expression than known methods using a single dsRNA, even at very low
CC concentrations. When dsRNA has at least one unpaired nucleotide at the
CC end, stability (and thus effective concentration in the cell) is improved
CC and efficiency can be increased further by pretreating the cells with
CC interferon. The present sequence is that of a target DNA of the invention
XX
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 99.0%; Score 577.2; DB 6; Length 582;
Best Local Similarity 99.5%; Pred. No. 2.8e-134;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db        1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy       61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
Db       61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy      121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
Db      121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy      181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db      181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy      241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
Db      241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy      301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
Db      301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy      361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
Db      361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy      421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
Db      421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy      481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
Db      481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy      541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
Db      541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
```

RESULT 5
ABX09972
ID ABX09972 standard; DNA; 582 BP.
XX
AC ABX09972;
XX
DT 23-JAN-2003 (first entry)
XX
DE Human bcl-w DNA fragment SEQ ID 37.
XX
KW Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;
KW prion; inhibition; human; ds.
XX
OS Homo sapiens.
XX
PN DE10100587-C1.
XX
PD 21-NOV-2002.
XX
PF 09-JAN-2001; 2001DE-01000587.
XX
PR 09-JAN-2001; 2001DE-01000587.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
DR WPI; 2002-742209/81.
XX
PT Inhibiting expression of target genes, e.g. oncogenes, in cells, by
PT introduction of complementary double-stranded oligoribonucleotide, after
PT treating the cell with interferon.
XX
PS Disclosure; Page 35-36; 98pp; German.
XX
CC This invention describes a novel method for inhibiting expression of a
CC target gene by introducing into the cell that contains the target gene at
CC least one oligoribonucleotide (dsRNAI) that has a double-stranded (ds)
CC structure of not more than 49 consecutive nucleotides (nt), where at
CC least a segment of one strand of the ds structure is complementary with
CC the target gene and the cells are treated with interferon before
CC introduction of dsRNAI. The method is used to inhibit expression of
CC target genes, particularly oncogenes, cytokine genes, Id (not defined)
CC protein genes; developmental or prion genes, or genes expressed in
CC pathogenic organisms (particularly plasmodia) or in viruses or viroids
CC (pathogenic in humans, animals or plants). Treating the cells with
CC interferon greatly increases the extent to which dsRNA can inhibit
CC expression of the target genes, and the effect is even greater when dsRNA
CC are modified to increase their stability. ABX09936-ABX10075 represent
CC gene fragments used to illustrate the method of the invention
XX
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 99.0%; Score 577.2; DB 6; Length 582;
Best Local Similarity 99.5%; Pred. No. 2.8e-134;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db        1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy       61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
Db       61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy      121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
Db      121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy      181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db      181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy      241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
Db      241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy      301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
Db      301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy      361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
Db      361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy      421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
```

```
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
```

RESULT 6
ABL91694
ID ABL91694 standard; DNA; 582 BP.
XX
AC ABL91694;
XX
DT 28-MAY-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 37.
XX
KW Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
KW Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
KW cytostatic; virucide; protozoacide; antibacterial; ds.
XX
OS Homo sapiens.
XX
PN DE10100586-C1.
XX
PD 11-APR-2002.
XX
PF 09-JAN-2001; 2001DE-01000586.
XX
PR 09-JAN-2001; 2001DE-01000586.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
DR WPI; 2002-270454/32.
XX
PT Inhibiting gene expression in cells, useful for e.g. treating tumors, by
PT introducing double-stranded complementary oligoRNA having unpaired
PT terminal bases.
XX
PS Claim 13; Page 32; 104pp; German.
XX
CC The invention relates to a method for inhibiting expression of a target
CC gene (ABL91658-ABL91797) in a cell by introducing at least one
CC oligoribonucleotide that has a double-stranded structure consisting of at
CC most 49 sequential nucleotide pairs, with at least part of one strand
CC complementary with the target gene and has at least one end a single-
CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for
CC antisense inhibition of gene expression useful e.g. for treating tumours
CC but the oligoribonucleotides may also be directed against genes present
CC in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans,
CC animals or plants) or against cytokine, Id, developmental or prion genes.
CC The method provides more effective inhibition of gene expression than use
CC of known oligonucleotides, probably because the unpaired overhang
CC increases stability and thus intracellular concentration
XX
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

  Query Match   99.0%; Score 577.2; DB 6; Length 582;
  Best Local Similarity   99.5%; Pred. No. 2.8e-134;
  Matches 579; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

```
Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
```

RESULT 7
ABT16642
ID ABT16642 standard; DNA; 3542 BP:
XX
AC ABT16642;
XX
DT 03-APR-2003 (first entry)
XX
DE Human bcl-2 gene SEQ ID No 4.
XX
KW Anti-tumour; DNAzyme; bcl-2 gene; tumour; malignant; chemotherapy;
KW radiation therapy; catalytic domain; enzyme; human; ds.
XX
OS Homo sapiens.
XX
PN WO200299090-A1.
XX
PD 12-DEC-2002.
XX
PF 07-JUN-2002; 2002WO-AU000739.
XX
PR 07-JUN-2001; 2001AU-00005527.
XX
PA (JOHJ) JOHNSON & JOHNSON RES PTY LTD.
XX
PI Sun L, Wang L, Turner RJ, Saravolac EG, Dass CR;
XX
DR WPI; 2003-140617/13.
XX
PT Novel DNAzyme useful for treating tumors, and for enhancing the
PT sensitivity of malignant or virus infected cells to therapy, comprises a
PT catalytic domain and binding domain contiguous to the catalytic domain.
XX
PS Disclosure; Page 44-45; 67pp; English.
XX
CC The invention relates to a DNAzyme which specifically cleaves mRNA
CC transcribed from a member of the bcl-2 gene family. The DNAzymes comprise

```
CC   a catalytic domain, binding domains contiguous with the 5' and 3' end of
CC   the catalytic domain, and therefore hybridise with, the two regions
CC   immediately flanking the purine residue of the cleavage site within the
CC   bcl-2 gene family mRNA, at which DNAzyme-catalysed cleavage is desired. A
CC   pharmaceutical composition comprising a DNAzyme of the invention is
CC   useful for treating tumours in a subject, and for enhancing the
CC   sensitivity of malignant or virus infected cells infected cells to
CC   therapy. The DNAzymes are useful in diagnostics, therapeutics,
CC   prophylaxis, research agents and in kits. The DNAzymes are also useful
CC   for increasing the susceptibility of tumour cells to anti-tumour
CC   therapies such as chemotherapy and radiation therapy. This polynucleotide
CC   sequence represents a human bcl-2 gene of the invention
XX
SQ   Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 U; 0 Other;

  Query Match             98.6%;  Score 575;  DB 8;  Length 3542;
  Best Local Similarity   99.1%;  Pred. No. 1.5e-133;
  Matches  578;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 236

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 296

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 356

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        357 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 416

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 476

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 536

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        537 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 596

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 656

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 716

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 583
              |||||||||||||||||||||||||||||||||||||||||||
Db        717 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 759


RESULT 8
AAX25132
ID   AAX25132 standard; DNA; 581 BP.
XX
AC   AAX25132;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Human bcl-w gene.
XX
KW   Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
KW   animal model; ss.
XX
OS   Homo sapiens.
XX
PN   WO9913710-A1.
XX
PD   25-MAR-1999.
XX
PF   16-SEP-1998;   98WO-AU000764.
XX
PR   16-SEP-1997;   97AU-00009228.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Cory S,  Adams J,  Print C,  Gibson L,  Koentgen F;
XX
DR   WPI; 1999-243890/20.
DR   P-PSDB; AAY05530.
XX
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w.
XX
PS   Claim 3; Page 32; 52pp; English.
XX
CC   The present sequence is the human bcl-w gene encoding Bcl-w protein (see
CC   AAY05530), a pro-survival member of the Bcl-2 family which is widely
CC   expressed and which is essential for spermatogenesis. The invention
CC   relates generally to a method of treatment and to an animal model for the
CC   identification of molecules and genetic sequences useful for inducing or
CC   reducing fertility of male animals. Methods are provided for the
CC   treatment of infertility, or for reducing fertility, by modulating
CC   spermatogenesis. An animal model carries a mutation is at least one
CC   allele of the human or murine bcl-w gene or in a gene associated with bcl
CC   -w. Such animals have disorganised seminferous tubules and are
CC   substantially infertile, but possess no other major abnormalities as
CC   determined by histological examination. They can be used to screen for
CC   therapeutic molecules including genetic sequences capable of inducing,
CC   enhancing or otherwise facilitating spermatogenesis in animals, or which
CC   can induce infertility
XX
SQ   Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 U; 0 Other;

  Query Match             98.3%;  Score 573;  DB 2;  Length 581;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-133;
  Matches  576;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
              |||||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
```

RESULT 9
AAV28334
ID AAV28334 standard; cDNA; 579 BP.
XX
AC AAV28334;
XX
DT 02-OCT-1998 (first entry)
XX
DE Human bcl-y gene.
XX
KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .579
FT /*tag= a
FT /product= "bcl-y"
FT /note= "No stop codon given"
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97US-00798897.
XX
PR 23-FEB-1996; 96US-0012201P.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1998-446079/38.
DR P-PSDB; AAW61392.
XX
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
PT recombinant protein for use in treating uncontrolled cell growth e.g.
PT cancers.
XX
PS Claim 3; Column 15/16; 27pp; English.
XX
CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2
CC family, components in the cell death pathway. The bcl-2 family have both
CC apoptotic activity and the apoptosis blocking activity. bcl-y falls in
CC the apoptosis activity category. The recombinant protein may be used to
CC prevent uncontrolled cell growth, either by its direct administration to
CC recombinant genetic constructs to increase its expression in vivo. Also,
CC antisense constructs can be used in disorders where prevention of cell
CC death is desired
XX
SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;

Query Match 97.4%; Score 567.8; DB 2; Length 579;
Best Local Similarity 98.8%; Pred. No. 6.3e-132;
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
              |||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
```

RESULT 10
AAX15946
ID AAX15946 standard; cDNA; 579 BP.
XX
AC AAX15946;
XX
DT 20-MAY-1999 (first entry)
XX
DE cDNA encoding the human bcl-y protein.
XX
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite;
KW ss.
XX
OS Homo sapiens.
XX
PN US5883229-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-00978523.
XX
PR 23-FEB-1996; 96US-0012201P.
PR 11-FEB-1997; 97US-00798897.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1999-214150/18.
DR P-PSDB; AAW97392.
XX

PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT modulating programmed cell death.
XX
PS Disclosure; Col 15-16; 26pp; English.
XX
CC The present sequence encodes human bcl-y protein (Hbcl-y). The
CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-
CC y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC - conditions where cells under go premature cell death as a result of
CC triggers which may or may not be apparent. They may also be used in this
CC way to develop cell lines which remain viable in culture for an extended
CC period. In contrast, if they act as cell death stimulators, Rbcl-y and
CC Hbcl-y may be used to treat conditions associated with prolonged cell
CC life span such as cancer (especially kaposi's sarcoma and lung cancer)
CC and auto/hyperimmune diseases. They may also be used to cause cell death
CC in, and hence control, parasites
XX
SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;

Query Match 97.4%; Score 567.8; DB 2; Length 579;
Best Local Similarity 98.8%; Pred. No. 6.3e-132;
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
              |||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
```

RESULT 11
ADB52996

ID ADB52996 standard; DNA; 582 BP.
XX
AC ADB52996;
XX
DT 04-DEC-2003 (first entry)
XX
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3538.
XX
KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
KW primary rat hepatocyte toxicity modelling; gene; ds.
XX
OS Rattus norvegicus.
XX
PN WO2003065993-A2.
XX
PD 14-AUG-2003.
XX
PF 04-FEB-2003; 2003WO-US003482.
XX
PR 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-0363534P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371150P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
PR 19-APR-2002; 2002US-0373602P.
PR 22-APR-2002; 2002US-0374139P.
PR 08-MAY-2002; 2002US-0378370P.
PR 09-MAY-2002; 2002US-0378652P.
PR 09-MAY-2002; 2002US-0378653P.
PR 09-MAY-2002; 2002US-0378665P.
PR 09-JUL-2002; 2002US-0394230P.
PR 09-JUL-2002; 2002US-0394253P.
PR 04-SEP-2002; 2002US-0407688P.
PR 28-JAN-2003; 2003US-0442900P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
PI Elashoff M;
XX
DR WPI; 2003-731472/69.
XX
PT Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT mean values.
XX
PS Claim 44; SEQ ID NO 3538; 874pp; English.
XX
CC The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
XX
SQ Sequence 582 BP; 111 A; 157 C; 200 G; 114 T; 0 U; 0 Other;

Query Match 90.5%; Score 527.6; DB 10; Length 582;
Best Local Similarity 94.2%; Pred. No. 6.9e-122;
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              |||||||||||||||||  |||||||||||||||||||| ||||| |||||||||||| |||
Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              |||||||||||||||||||||||||||||||||||| ||||| |||||||||||| |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              |||||||||||||||||||||||||||||||| ||||| |||||||||||||||||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              ||||| |||||||||||||| |||||||||||||||||||||||| ||||| || ||||||
Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              |||||||||||| |||||||||||||||||||||| || ||||| ||| ||||||||
Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||| ||||||||| || ||| |||||||||||||||||||||||||||||||
Db        361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
```

RESULT 12
AAV28333
ID AAV28333 standard; cDNA; 579 BP.
XX
AC AAV28333;
XX
DT 02-OCT-1998 (first entry)
XX
DE Rat bcl-y gene.
XX
KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS Rattus sp.
XX
FH Key   Location/Qualifiers
FT CDS   1. .579
FT   /*tag= a
FT   /product= "bcl-y"
FT   /note= "No stop codon given"
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97US-00798897.
XX
PR 23-FEB-1996; 96US-0012201P.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1998-446079/38.
DR P-PSDB; AAW61391.
XX
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
PT recombinant protein for use in treating uncontrolled cell growth e.g.
PT cancers.
XX
PS Claim 2; Column 13/14; 27pp; English.
XX
CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2
CC family, components in the cell death pathway. The bcl-2 family have both
CC apoptotic activity and the apoptosis blocking activity. bcl-y falls in
CC the apoptosis activity category. The recombinant protein may be used to
CC prevent uncontrolled cell growth, either by its direct administration to
CC recombinant genetic constructs to increase its expression in vivo. Also,
CC antisense constructs can be used in disorders where prevention of cell
CC death is desired
XX
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;

  Query Match   89.7%; Score 523; DB 2; Length 579;
  Best Local Similarity 94.0%; Pred. No. 9.6e-121;
  Matches 544; Conservative   0; Mismatches   35; Indels   0; Gaps   0;

```
Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              |||||||||||||||||  |||||||||||||||||||| ||||| |||||||||||| |||
Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              |||||||| ||||||||||||||||||||||||||| ||||| |||||||||||| |||
Db         61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              |||||||||||||||||||||||||||||||| ||||| |||||||||||||||||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              ||||| |||||||||||||| |||||||||||||||||||||||| ||||| || ||||||
Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              |||||||||||| |||||||||||||||||||||| || ||||| ||| ||||||||
Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||| ||||||||| || ||| |||||||||||||||||||||||||||||||
Db        361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
              |||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
```

RESULT 13
AAX15945
ID AAX15945 standard; cDNA; 579 BP.
XX
AC AAX15945;
XX
DT 20-MAY-1999 (first entry)

```
XX
DE   cDNA encoding the rat bcl-y protein.
XX
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite;
KW   ss.
XX
OS   Rattus sp.
XX
PN   US5883229-A.
XX
PD   16-MAR-1999.
XX
PF   25-NOV-1997;   97US-00978523.
XX
PR   23-FEB-1996;   96US-0012201P.
PR   11-FEB-1997;   97US-00798897.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1999-214150/18.
DR   P-PSDB; AAW97391.
XX
PT   Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT   modulating programmed cell death.
XX
PS   Disclosure; Col 13-16; 26pp; English.
XX
CC   The present sequence encodes rat bcl-y protein (Rbcl-y). The
CC   specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
CC   Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC   programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC   proteins may be used to treat conditions associated with a disruption of
CC   the cell death pathway. If they act as cell death inhibitors, they may be
CC   used in therapies to treat subjects suffering from: strokes, head trauma,
CC   Alzheimer's Disease, neural and muscular degenerative diseases
CC   (especially multiple sclerosis), myocardial infarction, vitally induced
CC   cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC   - conditions where cells under go premature cell death as a result of
CC   triggers which may or may not be apparent. They may also be used in this
CC   way to develop cell lines which remain viable in culture for an extended
CC   period. In contrast, if they act as cell death stimulators, Rbcl-y and
CC   Hbcl-y may be used to treat conditions associated with prolonged cell
CC   life span such as cancer (especially kaposi's sarcoma and lung cancer)
CC   and auto/hyperimmune diseases. They may also be used to cause cell death
CC   in, and hence control, parasites
XX
SQ   Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;

  Query Match             89.7%;  Score 523;  DB 2;  Length 579;
  Best Local Similarity   94.0%;  Pred. No. 9.6e-121;
  Matches  544;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              |||||||||||||||  ||||||||||||||||||||| ||||| |||||||||| |||
Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              |||||||  ||||||||||||||||||||||||||||| ||||| ||||||||||| |||
Db         61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              ||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||| ||||| ||||||| || |||||||||||||||||||||||||||||||||||
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              ||||| |||||||||||||| ||||||||||||||||||||||| |||| ||  ||||||
Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||| |||||||||||||||||||||||||||| || |||| ||||||||
Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||| ||||||||| ||||||||||||||| ||  ||| |||||||||||||||
Db        361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
              |||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579


RESULT 14
AAX25133
ID   AAX25133 standard; DNA; 581 BP.
XX
AC   AAX25133;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Mouse bcl-w gene.
XX
KW   Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
KW   animal model; ss.
XX
OS   Mus sp.
XX
PN   WO9913710-A1.
XX
PD   25-MAR-1999.
XX
PF   16-SEP-1998;   98WO-AU000764.
XX
PR   16-SEP-1997;   97AU-00009228.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Cory S,  Adams J,  Print C,  Gibson L,  Koentgen F;
XX
DR   WPI; 1999-243890/20.
DR   P-PSDB; AAY05531.
XX
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w.
XX
PS   Claim 3; Page 34; 52pp; English.
XX
CC   The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see
CC   AAY05531), a pro-survival member of the Bcl-2 family which is widely
CC   expressed and which is essential for spermatogenesis. The invention
CC   relates generally to a method of treatment and to an animal model for the
CC   identification of molecules and genetic sequences useful for inducing or
CC   reducing fertility of male animals. Methods are provided for the
CC   treatment of infertility, or for reducing fertility, by modulating
CC   spermatogenesis. An animal model carries a mutation is at least one
CC   allele of the human or murine bcl-w gene or in a gene associated with bcl
CC   -w. Such animals have disorganised seminferous tubules and are
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CC   substantially infertile, but possess no other major abnormalities as
CC   determined by histological examination. They can be used to screen for
CC   therapeutic molecules including genetic sequences capable of inducing,
CC   enhancing or otherwise facilitating spermatogenesis in animals, or which
CC   can induce infertility
XX
SQ   Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 U; 0 Other;

  Query Match             89.5%;  Score 521.8;  DB 2;  Length 581;
  Best Local Similarity   93.6%;  Pred. No. 1.9e-120;
  Matches  544;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              |||||||||||||||||  |||||||||||||||||||| ||||| |||||||||||| |||
Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              |||||||||||||||||||||||||||||||||||| ||||| |||||||| || |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              |||||||||||||||||||||||| |||||||| ||||| |||||||| ||||| |||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              ||||| |||||||||||||| |||||||||| |||||||||| ||||| || ||||||
Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||||| || ||||| ||  ||||||||
Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              ||||||||||| |||||||||||||||||||||| || |||||  ||||||||||||||||
Db        361 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT 15
AAT96578
ID   AAT96578 standard; DNA; 581 BP.
XX
AC   AAT96578;
XX
DT   22-APR-1998  (first entry)
XX
DE   Mouse bcl-w DNA.
XX
KW   Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW   diagnosis; degenerative disease; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .507
FT                   /*tag= a
FT                   /product= "bcl-w"
FT                   /note= "q"
XX
PN   WO9735971-A1.
XX
PD   02-OCT-1997.
XX
PF   27-MAR-1997;   97WO-AU000199.
XX
PR   27-MAR-1996;   96AU-00008965.
XX
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI   Cory S,  Adams JM,  Gibson LM,  Holmgreen SP;
XX
DR   WPI; 1997-489635/45.
DR   P-PSDB; AAW36048.
XX
PT   Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
PT   inhibit cell survival, e.g. for treatment of cancer and degenerative
PT   diseases.
XX
PS   Claim 3; Page 50-51; 86pp; English.
XX
CC   This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene
CC   family. This gene promotes cell survival, so its modulation is useful in
CC   treatment of cancer or auto-immune diseases, degenerative diseases (e.g.
CC   stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,
CC   hypoxia, ischaemia, human immunodeficiency virus infection or in cell
CC   transplants. Up-regulation of the gene can also be used to modify cell
CC   lines cultured in vivo, e.g. to develop new lines, to facilitate
CC   isolation of hybridomas and to increase survival of primary explants
CC   during genetic modification. It can be used to produce recombinant Bcl-w
CC   for therapy, diagnosis, antibody production or screening of potential
CC   modulators
XX
SQ   Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 U; 0 Other;

  Query Match             85.9%;  Score 501;  DB 2;  Length 581;
  Best Local Similarity   91.4%;  Pred. No. 3e-115;
  Matches  531;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              ||| |||||||||||||  |||||||||||| ||||| ||||| |||||||||||| |||
Db          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              |||||||||||||||||||||||| |||||||| ||||| |||||||| ||||| |||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||| |||||||||||||| |||||||||| |||||||||| ||||| || ||||||
Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||||| || ||||| ||  ||||||||
Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              ||||| ||||| ||||| |||||||||||||||||| || ||||  ||||||||||||||||
Db        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||| |||||||||| |||||||||||||||||||||||||||||||||| || |||
Db        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Db          481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540

Qy          541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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Db          541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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Search completed: April 10, 2005, 16:55:35
Job time : 462.785 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 16:31:16 ; Search time 144.247 Seconds
(without alignments)
6613.285 Million cell updates/sec

Title: US-09-925-674B-6
Perfect score: 583
Sequence: 1 atggcgaccccagcctcggc.....ctttttgctagcaagtgaa 583

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	583	100.0	583	4	US-09-155-327G-6	Sequence 6, Appli
2	572.4	98.2	582	4	US-09-949-016-5057	Sequence 5057, Ap
3	567.8	97.4	579	1	US-08-798-897-2	Sequence 2, Appli
4	567.8	97.4	579	2	US-08-978-523-2	Sequence 2, Appli
5	523	89.7	579	1	US-08-798-897-1	Sequence 1, Appli
6	523	89.7	579	2	US-08-978-523-1	Sequence 1, Appli
7	501	85.9	581	4	US-09-155-327G-8	Sequence 8, Appli
8	424	72.7	1098	4	US-09-010-147B-23	Sequence 23, Appl
9	423.6	72.7	1864	3	US-09-149-476-130	Sequence 130, App
10	423.4	72.6	5199	4	US-09-949-016-16799	Sequence 16799, A
11	414.6	71.1	601	4	US-09-949-016-177003	Sequence 177003,
12	131	22.5	926	1	US-08-081-448-5	Sequence 5, Appli
13	131	22.5	926	2	US-08-470-670A-6	Sequence 6, Appli
14	131	22.5	926	3	US-08-481-739-1	Sequence 1, Appli
15	131	22.5	926	3	US-09-167-921-1	Sequence 1, Appli
16	131	22.5	926	3	US-09-277-020-39	Sequence 39, Appl
17	131	22.5	926	3	US-09-323-743-1	Sequence 1, Appli
18	131	22.5	926	3	US-08-461-511A-6	Sequence 6, Appli
19	131	22.5	926	3	US-09-271-014A-5	Sequence 5, Appli
20	131	22.5	926	4	US-09-023-655-1430	Sequence 1430, Ap
21	131	22.5	926	4	US-09-814-915A-106	Sequence 106, App
22	131	22.5	926	5	PCT-US94-07089-6	Sequence 6, Appli
23	131	22.5	1236	4	US-09-639-245-1	Sequence 1, Appli
24	127.6	21.9	1455	4	US-09-639-245-7	Sequence 7, Appli
25	125	21.4	711	4	US-09-741-238-1	Sequence 1, Appli
26	123.4	21.2	717	2	US-08-465-485A-20	Sequence 20, Appl
27	123.4	21.2	717	3	US-09-080-285-20	Sequence 20, Appl
28	123.4	21.2	4825	6	5459251-1	Patent No. 5459251
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30	123.4	21.2	5086	2	US-08-465-485A-19	Sequence 19, Appl
31	123.4	21.2	5086	2	US-08-365-486A-14	Sequence 14, Appl
32	123.4	21.2	5086	3	US-09-080-285-19	Sequence 19, Appl
33	123.4	21.2	5086	3	US-08-880-342-14	Sequence 14, Appl
34	123.4	21.2	5086	3	US-09-724-426-19	Sequence 19, Appl
35	123.4	21.2	5086	3	US-09-233-527-7	Sequence 7, Appli
36	123.4	21.2	5086	5	PCT-US93-05651-4	Sequence 4, Appli
37	123.4	21.2	5086	5	PCT-US93-06251-2	Sequence 2, Appli
38	123.4	21.2	5094	3	US-09-234-186-7	Sequence 7, Appli
39	123.4	21.2	5104	6	5506344-1	Patent No. 5506344
40	123.4	21.2	5104	6	5506344-1	Patent No. 5506344
41	123.2	21.1	60489	4	US-09-949-016-16287	Sequence 16287, A
42	121.8	20.9	760	1	US-08-405-702A-11	Sequence 11, Appl
43	121.8	20.9	6030	4	US-09-023-655-1015	Sequence 1015, Ap
44	120.4	20.7	1384	4	US-08-899-367-1	Sequence 1, Appli
45	120.2	20.6	1846	2	US-08-365-486A-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-155-327G-6
; Sequence 6, Application US/09155327G
; Patent No. 6790637
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 2096584
; CURRENT APPLICATION NUMBER: US/09/155,327G
; CURRENT FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 583
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(579)
US-09-155-327G-6

Query Match 100.0%; Score 583; DB 4; Length 583;
Best Local Similarity 100.0%; Pred. No. 1.7e-144;
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 583
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RESULT 2
US-09-949-016-5057
; Sequence 5057, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5057
;   LENGTH: 582
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5057

  Query Match             98.2%;  Score 572.4;  DB 4;  Length 582;
  Best Local Similarity   99.0%;  Pred. No. 1.1e-141;
  Matches  576;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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RESULT 3
US-08-798-897-2
; Sequence 2, Application US/08798897
; Patent No. 5789201
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  579 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-798-897-2

  Query Match             97.4%;  Score 567.8;  DB 1;  Length 579;
  Best Local Similarity   98.8%;  Pred. No. 1.8e-140;
  Matches  572;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT 60
Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
Db        121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
              |||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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RESULT 4
US-08-978-523-2
; Sequence 2, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-08-978-523-2

Query Match 97.4%; Score 567.8; DB 2; Length 579;
Best Local Similarity 98.8%; Pred. No. 1.8e-140;
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
              |||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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RESULT 5
US-08-798-897-1
; Sequence 1, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.

```
;       REGISTRATION NUMBER:  32,893
;       REFERENCE/DOCKET NUMBER:  1483.0140001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  579 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  both
;       TOPOLOGY:  both
;     MOLECULE TYPE:  cDNA
US-08-798-897-1 .

  Query Match             89.7%;  Score 523;  DB 1;  Length 579;
  Best Local Similarity   94.0%;  Pred. No. 1.2e-128;
  Matches  544;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              |||||||||||||||||  |||||||||||||||||| |||||  |||||||||||  |||
Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||  ||||||||||||||||||||||||||||||  |||||  ||||||||||| |||
Db         61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              |||||||||||||||||||||||||||||||||  |||||  |||||||||||||||||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||||  |||||  ||||||||  ||  ||||||||||||||||||||||||||||||
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||  |||||||||||||  ||||||||||||||||||||||||  |||||  ||  ||||||
Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||  ||||||||||||||||||||||  ||  |||||  |||  ||||||||
Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              ||||||||||  |||||||||  ||||||||||||  ||  |||  ||||||||||||||||
Db        361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
              |||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579


RESULT 6
US-08-978-523-1
; Sequence 1, Application US/08978523
; Patent No. 5883229
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,523
;      FILING DATE:  herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  579 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-978-523-1

  Query Match             89.7%;  Score 523;  DB 2;  Length 579;
  Best Local Similarity   94.0%;  Pred. No. 1.2e-128;
  Matches  544;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              |||||||||||||||||  |||||||||||||||||| |||||  |||||||||||  |||
Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||  ||||||||||||||||||||||||||||||  |||||  ||||||||||| |||
Db         61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              |||||||||||||||||||||||||||||||||  |||||  |||||||||||||||||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||||  |||||  ||||||||  ||  ||||||||||||||||||||||||||||||
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||  |||||||||||||  ||||||||||||||||||||||||  |||||  ||  ||||||
Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||  ||||||||||||||||||||||  ||  |||||  |||  ||||||||
Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              ||||||||||  |||||||||  ||||||||||||  ||  |||  ||||||||||||||||
Db        361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579


RESULT 7
US-09-155-327G-8
; Sequence 8, Application US/09155327G
; Patent No. 6790637
; GENERAL INFORMATION:
;  APPLICANT: AMRAD Operations Pty Ltd
;  TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
;  TITLE OF INVENTION:  FAMILY OF APOPTOSIS-CONTROLLING GENES
;  FILE REFERENCE: 2096584
;  CURRENT APPLICATION NUMBER: US/09/155,327G
;  CURRENT FILING DATE:  1999-03-29
;  PRIOR APPLICATION NUMBER: PN8965
;  PRIOR FILING DATE: 1996-03-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 581
;   TYPE: DNA
;   ORGANISM: Mouse
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(579)
US-09-155-327G-8

  Query Match             85.9%;  Score 501;  DB 4;  Length 581;
  Best Local Similarity   91.4%;  Pred. No. 8e-123;
  Matches  531;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Db          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              |||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||||| || ||||| ||  ||||||||
Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Db        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||| |||||||||| |||||||||||||||||||||||||||||||| || |||
Db        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              |||||||||||||| |||||||||| |||||| |||||| ||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
              |||||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT 8
US-09-010-147B-23
; Sequence 23, Application US/09010147B
; Patent No. 6653445
;   GENERAL INFORMATION:
;        APPLICANT: Ni et al.
;        TITLE OF INVENTION: Human Proteins
;        NUMBER OF SEQUENCES: 24
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: MD
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC
;                       compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/010,147B
;             FILING DATE: 12-No. 6653445-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 60/034,205
;             FILING DATE: 21-JAN-1997
;             APPLICATION NUMBER: US 60/034,204
;             FILING DATE: 21-JAN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Jonathan L. Klein
;             REGISTRATION NUMBER: 41,119
;             REFERENCE/DOCKET NUMBER: PF353
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 301-309-8504
;             TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 23:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1098 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1095
;        SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-010-147B-23

  Query Match             72.7%;  Score 424;  DB 4;  Length 1098;
  Best Local Similarity   98.8%;  Pred. No. 2.2e-102;
  Matches  427;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGG 432
              ||||||||||||
Db        421 AGTGGGGGCTGG 432
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RESULT 9
US-09-149-476-130
; Sequence 130, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
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; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,492
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; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
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; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,878
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
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; EARLIER APPLICATION NUMBER: 60/056,879
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; EARLIER APPLICATION NUMBER: 60/056,880
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; EARLIER APPLICATION NUMBER: 60/056,894
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; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910

; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 72.7%; Score 423.6; DB 3; Length 1864;
Best Local Similarity 98.6%; Pred. No. 3.3e-102;
Matches 426; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 70

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 130

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        131 CCGCTGCACCAAGCCATGCGGGCAGCKGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 190

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 250

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        251 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 310

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 370

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db        371 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 430

Qy        421 AGTGGGGGCTGG 432
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Db        431 AGTGGGGGCTGG 442
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RESULT 10
US-09-949-016-16799
; Sequence 16799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16799
; LENGTH: 5199
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16799

Query Match 72.6%; Score 423.4; DB 4; Length 5199;
Best Local Similarity 98.6%; Pred. No. 5.3e-102;
Matches 427; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2001 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 2060

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2061 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 2120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 2180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       2181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 2240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 2300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 2360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db       2361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 2420

Qy        421 AGTGGGGGCTGGG 433
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Db       2421 AGTGGGGGCTGGG 2433
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RESULT 11
US-09-949-016-177003
; Sequence 177003, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 177003
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-177003

Query Match 71.1%; Score 414.6; DB 4; Length 601;
Best Local Similarity 98.6%; Pred. No. 5.4e-100;
Matches 417; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 238

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 298

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 CCRCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 358

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        359 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 418

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 478

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Db        479 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 538

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db        539 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 598

Qy        421 AGT 423
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Db        599 AGT 601
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RESULT 12
US-08-081-448-5
; Sequence 5, Application US/08081448
; Patent No. 5646008
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5646008th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,448
; FILING DATE: 19930622
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646008thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-744-0090
; TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
US-08-081-448-5

Query Match 22.5%; Score 131; DB 1; Length 926;
Best Local Similarity 56.3%; Pred. No. 5.3e-25;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

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Qy         98 CCGGGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGT 157
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Db        364 CCCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAGCGCTGAGGGAGGCAGGCGACGAGT 423

Qy        158 TCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAG 217
              | ||    || | ||||||  | |||  ||| ||| |  | |||||  |  | |||||||
Db        424 TTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 483

Qy        218 GCTCAGCCCAGCAACGCTTCACCCAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACT 277
              | ||||  | ||  ||||    |||||      | ||||| || |  |  ||     ||||
Db        484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACT 543
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Qy        278 GGGGCCGCCTTGTAGCCTTCTTTCTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACA 337
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Db        544 GGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTAGACA 603

Qy        338 AGGAGATGGAACCACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGC 397
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Qy        518 TGCTGACGGGGGCCG 532
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Db        784 GCATGACTGTGGCCG 798
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RESULT 13
US-08-470-670A-6
; Sequence 6, Application US/08470670A
; Patent No. 5834309
; Patent No. 5834309 5710045
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B. B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,670A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,448
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:090--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
US-08-470-670A-6

Query Match 22.5%; Score 131; DB 2; Length 926;
Best Local Similarity 56.3%; Pred. No. 5.3e-25;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

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Qy         98 CCGGGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGT 157
              || |||||       |   |   |  | | |||||  || |||  || || || ||||
Db        364 CCCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAGCGCTGAGGGAGGCAGGCGACGAGT 423

Qy        158 TCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAG 217
              | ||   || | ||||||  | |||  ||| ||| |  | |||||  ||  | |||||||
Db        424 TTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 483

Qy        218 GCTCAGCCCAGCAACGCTTCACCCAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACT 277
              |  ||||  | ||  ||||    |||||      | |||||  ||  |  ||    ||||
Db        484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACT 543

Qy        278 GGGGCCGCCTTGTAGCCTTCTTTCTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACA 337
              |||| ||| |||| ||||| ||   ||| || | |||||||| | || || ||  |||
Db        544 GGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTAGACA 603

Qy        338 AGGAGATGGAACCACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGC 397
              |||||||| |   | ||||| | |   |   | |||||||  |||||| |     |
Db        604 AGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 663

Qy        398 GGCTGGTCGACTGGATCCACAGCAGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGG 457
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Qy        458 ACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAG 517
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Db        784 GCATGACTGTGGCCG 798
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RESULT 14
US-08-481-739-1
; Sequence 1, Application US/08481739
; Patent No. 6143291
; GENERAL INFORMATION:
; APPLICANT: June, Carl H. and Thompson, Craig B.
; TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
; TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,739
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,518
; FILING DATE: 04-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. (GAD)
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RPI-034CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;        NAME/KEY:  CDS
;        LOCATION:  135..836
US-08-481-739-1

  Query Match              22.5%;  Score 131;  DB 3;  Length 926;
  Best Local Similarity    56.3%;  Pred. No. 5.3e-25;
  Matches  245;  Conservative    0;  Mismatches  190;  Indels    0;  Gaps    0;

Qy         98 CCGGGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGT 157
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Qy        158 TCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAG 217
Db        424 TTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 483

Qy        218 GCTCAGCCCAGCAACGCTTCACCCAGGTCTCCGACGAACTTTTCAAGGGGGCCCCAACT 277
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Qy        338 AGGAGATGGAACCACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGC 397
Db        604 AGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 663

Qy        398 GGCTGGTCGACTGGATCCACAGCAGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGG 457
Db        664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGTGGAACTCTATGGGA 723

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Qy        518 TGCTGACGGGGGCCG 532
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RESULT 15
US-09-167-921-1
; Sequence 1, Application US/09167921A
; Patent No. 6172216
; GENERAL INFORMATION:
;  APPLICANT: Bennett, C. Frank
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Nickoloff, Brian J.
;  APPLICANT: Zhang, QingQing
;  TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
;  FILE REFERENCE: ISPH-0324
;  CURRENT APPLICATION NUMBER: US/09/167,921A
;  CURRENT FILING DATE: 1998-10-07
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 926
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (135)..(836)
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: L20121 Genbank
;   DATABASE ENTRY DATE: 1994-07-26
US-09-167-921-1

  Query Match              22.5%;  Score 131;  DB 3;  Length 926;
  Best Local Similarity    56.3%;  Pred. No. 5.3e-25;
  Matches  245;  Conservative    0;  Mismatches  190;  Indels    0;  Gaps    0;

Qy         98 CCGGGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGT 157
Db        364 CCCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAGCGCTGAGGGAGGCAGGCGACGAGT 423

Qy        158 TCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAG 217
Db        424 TTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 483

Qy        218 GCTCAGCCCAGCAACGCTTCACCCAGGTCTCCGACGAACTTTTCAAGGGGGCCCCAACT 277
Db        484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACT 543

Qy        278 GGGGCCGCCTTGTAGCCTTCTTTCTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACA 337
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Qy        398 GGCTGGTCGACTGGATCCACAGCAGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGG 457
Db        664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGTGGAACTCTATGGGA 723

Qy        458 ACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAG 517
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Job time : 146.247 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 18:38:08 ; Search time 500.358 Seconds
(without alignments)
7060.905 Million cell updates/sec

Title: US-09-925-674B-6
Perfect score: 583
Sequence: 1 atggcgaccccagcctcggc.....ctttttgctagcaagtgaa 583

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	578.2	99.2	583	9	US-09-925-674A-6	Sequence 6, Appli
2	577.2	99.0	582	18	US-10-384-339C-37	Sequence 37, Appl
3	572.4	98.2	582	19	US-10-479-832A-4	Sequence 4, Appli
4	519.6	89.1	582	9	US-09-925-674A-8	Sequence 8, Appli
5	423.6	72.7	1864	10	US-09-809-391-130	Sequence 130, App
6	423.6	72.7	1864	10	US-09-882-171-130	Sequence 130, App
7	423.6	72.7	1864	17	US-10-164-861-130	Sequence 130, App
8	423.4	72.6	578	16	US-10-029-386-10549	Sequence 10549, A
9	422.4	72.5	433	16	US-10-029-386-24249	Sequence 24249, A
10	255.4	43.8	6049	15	US-10-311-455-201	Sequence 201, App
c 11	219.8	37.7	6049	15	US-10-311-455-202	Sequence 202, App
12	152	26.1	590	16	US-10-029-386-13384	Sequence 13384, A
13	151	25.9	151	16	US-10-029-386-27084	Sequence 27084, A
14	150	25.7	150	9	US-09-864-761-17690	Sequence 17690, A
15	145.2	24.9	660	17	US-10-402-017-9	Sequence 9, Appli
16	144.2	24.7	600	17	US-10-402-017-7	Sequence 7, Appli
17	141.2	24.2	540	17	US-10-402-017-5	Sequence 5, Appli
18	136.2	23.4	660	17	US-10-402-017-11	Sequence 11, Appl
19	136.2	23.4	863	17	US-10-402-017-3	Sequence 3, Appli
20	132.8	22.8	1466	18	US-10-283-975A-394	Sequence 394, App
21	131	22.5	636	16	US-10-169-223-13	Sequence 13, Appl
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24	131	22.5	926	9	US-09-734-847A-39	Sequence 39, Appl
25	131	22.5	926	9	US-09-952-278-5	Sequence 5, Appli
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29	131	22.5	926	17	US-10-641-643-1430	Sequence 1430, Ap
30	131	22.5	926	18	US-10-717-597-87	Sequence 87, Appl
31	131	22.5	926	18	US-10-776-827-106	Sequence 106, App
32	131	22.5	926	18	US-10-825-282-47	Sequence 47, Appl
33	131	22.5	926	19	US-10-479-832A-3	Sequence 3, Appli
34	131	22.5	1236	18	US-10-792-517-1	Sequence 1, Appli
35	129.8	22.3	1748	17	US-10-388-934-539	Sequence 539, App
36	129.8	22.3	1748	17	US-10-191-803-202	Sequence 202, App
37	127.6	21.9	1455	18	US-10-792-517-7	Sequence 7, Appli
38	126.6	21.7	711	13	US-10-087-192-1952	Sequence 1952, Ap
39	125	21.4	720	17	US-10-148-953A-8	Sequence 8, Appli
40	123.4	21.2	717	16	US-10-053-645A-20	Sequence 20, Appl
41	123.4	21.2	720	17	US-10-148-953A-6	Sequence 6, Appli
42	123.4	21.2	720	17	US-10-148-953A-7	Sequence 7, Appli
43	123.4	21.2	720	17	US-10-297-321-1	Sequence 1, Appli
44	123.4	21.2	931	18	US-10-714-310-18	Sequence 18, Appl
45	123.4	21.2	5086	8	US-08-726-211-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-925-674A-6
; Sequence 6, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 583
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(579)
US-09-925-674A-6

Query Match 99.2%; Score 578.2; DB 9; Length 583;
Best Local Similarity 99.5%; Pred. No. 1.2e-156;
Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Qy       181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy       241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Qy       361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Qy       421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Qy       481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Qy       541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 583
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RESULT 2
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; Sequence 37, Application US/10384339C
; Publication No. US20040175703A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Roland
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE
; FILE REFERENCE: 20200/2002
; CURRENT APPLICATION NUMBER: US/10/384,339C
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: DE 10155280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 10158411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 10160151.4
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: bcl-w
; PATENT DOCUMENT NUMBER: U59747
US-10-384-339C-37

Query Match 99.0%; Score 577.2; DB 18; Length 582;
Best Local Similarity 99.5%; Pred. No. 2.3e-156;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Qy       181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db       181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy       241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
Db       241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy       301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
Db       301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy       361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
Db       361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy       421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
Db       421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy       481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
Db       481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy       541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
Db       541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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RESULT 3
US-10-479-832A-4
; Sequence 4, Application US/10479832A
; Publication No. US20050064407A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson Research Pty Ltd
; TITLE OF INVENTION: bcl-2 DNAzymes
; FILE REFERENCE: WJP13107942
; CURRENT APPLICATION NUMBER: US/10/479,832A
; CURRENT FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-479-832A-4

Query Match 98.2%; Score 572.4; DB 19; Length 582;
Best Local Similarity 99.0%; Pred. No. 5.5e-155;
Matches 576; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy         1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db         1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy        61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
Db        61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy       121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
Db       121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||| |||||  ||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCAGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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RESULT 4
US-09-925-674A-8
; Sequence 8, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(579)
US-09-925-674A-8

Query Match 89.1%; Score 519.6; DB 9; Length 582;
Best Local Similarity 93.3%; Pred. No. 9.1e-140;
Matches 543; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              |||||||||||||||||  |||||||||||||||||| ||||| |||||||||||  |||
Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              | |||||||||||||||||||||||||||||||||||| ||||| |||||||| ||  |||
Db         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              |||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||  |||||||||||||||| |||||||||| |||||||||| ||||| || |||||||
Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||||||| || ||||| ||  ||||||||
Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||| |||||||||||||||||||||||| || ||||  ||||||||||||||||
Db        361 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        421 AGTGGCGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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RESULT 5
US-09-809-391-130
; Sequence 130, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1648)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-809-391-130

Query Match 72.7%; Score 423.6; DB 10; Length 1864;
Best Local Similarity 98.6%; Pred. No. 4.7e-112;
Matches 426; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 70

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 130

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              |||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db        131 CCGCTGCACCAAGCCATGCGGGCAGCKGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 190

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 250

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Db        251 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 310

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 370

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db        371 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 430

Qy        421 AGTGGGGGCTGG 432
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Db        431 AGTGGGGGCTGG 442
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RESULT 6
US-09-882-171-130
; Sequence 130, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
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; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
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; PRIOR APPLICATION NUMBER: 60/047,583
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; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/047,612
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; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,674
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,669
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,312
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; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/056,886
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; PRIOR APPLICATION NUMBER: 60/056,911

; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,636
; PRIOR FILING DATE: 1997-08-22
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; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
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; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match 72.7%; Score 423.6; DB 10; Length 1864;
Best Local Similarity 98.6%; Pred. No. 4.7e-112;
Matches 426; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Qy    1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db   11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 70

Qy   61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
Db   71 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 130

Qy  121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
Db  131 CCGCTGCACCAAGCCATGCGGGCAGCKGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 190

Qy  181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db  191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 250

Qy  241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
Db  251 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 310

Qy  301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
Db  311 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 370

Qy  361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
Db  371 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 430

Qy  421 AGTGGGGGCTGG 432
Db  431 AGTGGGGGCTGG 442
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RESULT 7
US-10-164-861-130
; Sequence 130, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1648)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-164-861-130

Query Match 72.7%; Score 423.6; DB 17; Length 1864;
Best Local Similarity 98.6%; Pred. No. 4.7e-112;
Matches 426; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Qy    1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db   11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 70

Qy   61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
Db   71 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 130
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Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
Db        131 CCGCTGCACCAAGCCATGCGGGCAGCKGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 190
Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 250
Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
Db        251 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 310
Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
Db        311 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 370
Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
Db        371 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 430
Qy        421 AGTGGGGGCTGG 432
Db        431 AGTGGGGGCTGG 442
```

RESULT 8
US-10-029-386-10549
; Sequence 10549, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10549
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 0.00e+00
; OTHER INFORMATION: NT HIT: gi14751151, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALUE 2.00e-72
US-10-029-386-10549

Query Match 72.6%; Score 423.4; DB 16; Length 578;
Best Local Similarity 98.6%; Pred. No. 4.9e-112;
Matches 427; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db        105 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 164
Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
Db        165 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 224
Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
Db        225 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 284
```

```
Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        285 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 344
Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
Db        345 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 404
Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
Db        405 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 464
Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
Db        465 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCAGCTGGCTGACTGGATCCACAGC 524
Qy        421 AGTGGGGGCTGGG 433
Db        525 AGTGGGGGCTGGG 537
```

RESULT 9
US-10-029-386-24249
; Sequence 24249, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24249
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALUE 2.00e-72
; OTHER INFORMATION: NT HIT: gi14751151, EVALUE 0.00e+00
US-10-029-386-24249

Query Match 72.5%; Score 422.4; DB 16; Length 433;
Best Local Similarity 98.6%; Pred. No. 9.3e-112;
Matches 426; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db          2 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 61
Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
Db         62 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 121
Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
Db        122 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 181
Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        182 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 241
```

```
Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
Db        242 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 301

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
Db        302 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 361

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
Db        362 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCAGCTGGCTGACTGGATCCACAGC 421

Qy        421 AGTGGGGGCTGG 432
Db        422 AGTGGGGGCTGG 433


RESULT 10
US-10-311-455-201
; Sequence 201, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 201
;   LENGTH: 6049
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-201

  Query Match             43.8%;  Score 255.4;  DB 15;  Length 6049;
  Best Local Similarity   74.4%;  Pred. No. 1.6e-63;
  Matches  322;  Conservative    0;  Mismatches  111;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db       5001 ATGGCGATTTTAGTTTCGGTTTTAGATATACGGGTTTTGGTGGTAGATTTTGTAGGTTAT 5060

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
Db       5061 AAGTTGAGGTAGAAGGGTTATGTTTGTGGAGTTGGTTTCGGGGAGGGTTTAGTAGTTGAT 5120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
Db       5121 TCGTTGTATTAAGTTATGCGGGTAGTTGGAGATGAGTTCGAGATTCGTTTTCGGCGTATT 5180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db       5181 TTTTTTGATTTGGCGGTTTAGTTGTATGTGATTTTAGGTTTAGTTTAATAACGTTTTATT 5240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
Db       5241 TAGGTTTTCGATGAATTTTTTTAAGGGGGTTTTAATTGGGGTCGTTTTGTAGTTTTTTTT 5300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
Db       5301 GTTTTTGGGGTTGTATTGTGTGTTGAGAGTGTTAATAAGGAGATGGAATTATTGGTGGGA 5360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
Db       5361 TAAGTGTAGGAGTGGATGGTGGTTTATTTGGAGACGTAGTTGGTTGATTGGATTTATAGT 5420

Qy        421 AGTGGGGGCTGGG 433
Db       5421 AGTGGGGGTTGGG 5433


RESULT 11
US-10-311-455-202/c
; Sequence 202, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 202
;   LENGTH: 6049
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-202

  Query Match             37.7%;  Score 219.8;  DB 15;  Length 6049;
  Best Local Similarity   70.0%;  Pred. No: 2.9e-53;
  Matches  296;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db       1049 ATAACGACCCCAACCTCGACCCCAAACACACGAACTCTAATAACAAACTTTATAAATTAT 990

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
Db        989 AAACTAAAACAAAAAAATTATATCTATAAAACTAACCCCGAAAAAAACCCAACAACTAAC 930

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
Db        929 CCGCTACACCAAACCATACGAACAACTAAAAATAAATTCGAAACCCGCTTCCGACGCACC 870

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        869 TTCTCTAATCTAACGACTCAACTACATATAACCCCAAACTCAACCCAACAACGCTTCACC 810

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
Db        809 CAAATCTCCGATAAACTTTTTCAAAAAAACCCCAACTAAAACCGCCTTATAACCTTCTTT 750

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
Db        749 ATCTTTAAAACTACACTATATACTAAAAATATCAACAAAAAAATAAAACCACTAATAAAA 690

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
Db        689 CAAATACAAAAATAAATAATAACCTACCTAAAAACGCAACTAACTAACTAAATCCACAAC 630

Qy        421 AGT 423
Db        629 AAT 627
```

```
RESULT 12
US-10-029-386-13384
; Sequence 13384, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13384
;   LENGTH: 590
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR14.3
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
;   OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 2.00e-10
;   OTHER INFORMATION: NT HIT: gi14751151, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 1.00e-119
US-10-029-386-13384

  Query Match             26.1%;  Score 152;  DB 16;  Length 590;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-34;
  Matches  152;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        432 GGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGA 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 GGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGA 84

Qy        492 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGT 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGT 144

Qy        552 AACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 583
              ||||||||||||||||||||||||||||||
Db        145 AACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 176


RESULT 13
US-10-029-386-27084
; Sequence 27084, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27084
;   LENGTH: 151
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR14.3
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
;   OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 5.00e-70
;   OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11
;   OTHER INFORMATION: NT HIT: gi14574571, EVALUE 9.00e-80
US-10-029-386-27084

  Query Match             25.9%;  Score 151;  DB 16;  Length 151;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-33;
  Matches  151;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        432 GGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGA 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGA 60

Qy        492 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGT 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGT 120

Qy        552 AACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
              |||||||||||||||||||||||||||||
Db        121 AACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 151


RESULT 14
US-09-864-761-17690
; Sequence 17690, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 17690
;   LENGTH: 150
```

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;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL049829.2
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.5
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.9
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL =  1
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
;   OTHER INFORMATION: NT HIT: D87461.1, EVALUE 2.00e-79
;   OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 8.00e-70
;   OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11
US-09-864-761-17690

  Query Match            25.7%;  Score 150;  DB 9;  Length 150;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-33;
  Matches  150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       433 GCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGAG 492
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 GCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGAG 60

Qy       493 GGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGTA 552
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGTA 120

Qy       553 ACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
            ||||||||||||||||||||||||||||||
Db       121 ACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 150


RESULT 15
US-10-402-017-9
; Sequence 9, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
;  APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
;  TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
;  TITLE OF INVENTION:  such cells
;  FILE REFERENCE: Case 1/1314
;  CURRENT APPLICATION NUMBER: US/10/402,017
;  CURRENT FILING DATE:  2003-03-28
;  PRIOR APPLICATION NUMBER: US 60/369,307
;  PRIOR APPLICATION NUMBER: April 2, 2002
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 660
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Deletion mutant of SEQ ID NO:3 (del66-83)
US-10-402-017-9

  Query Match            24.9%;  Score 145.2;  DB 17;  Length 660;
  Best Local Similarity  58.2%;  Pred. No. 7.7e-32;
  Matches  255;  Conservative    0;  Mismatches  183;  Indels    0;  Gaps    0;

Qy        95 GCCCCGGGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGAGATG 154
            |||||| ||  |   | |||||  |   |  |  | |||||  || | |  || || ||||
Db       185 GCCCCGCGGTAGCGGCCGCAGCAGCAGCCGTAAAGCAAGCGCTGAGAGAGGCCGGCGATG 244

Qy       155 AGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCAGCTGCATGTGACCC 214
            ||||  |||   || | ||||||  | |||  ||||||  |  | |||||  ||| | ||||
Db       245 AGTTTGAGCTGCGGTACCGGCGGGCGTTCAGTGATCTAACATCCCAGCTTCATATAACCC 304

Qy       215 CAGGCTCAGCCCAGCAACGCTTCACCCAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCA 274
            ||||  | ||  | ||| ||||    |||||     | ||||| || |  |  ||    |

Db       305 CAGGGACTGCATATCAAAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAA 364

Qy       275 ACTGGGGCCGCCTTGTAGCCTTCTTTCTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCA 334
            ||||||| ||| |||| ||||| ||   ||| || |  || || ||||  || || ||
Db       365 ACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCGGTGGAGCCCTCTGTGTGGAAAGCGTAG 424

Qy       335 ACAAGGAGATGGAACCACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGA 394
            |||||||||||| |   | ||||| | |   |       |||||||   |||||||| |
Db       425 ACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAAGTTGGATGGCCACCTACCTGAATG 484

Qy       395 CGCGGCTGGTCGACTGGATCCACAGCAGTGGGGGCTGGGCGGAGTTCACAGCTCTATACG 454
                | || |      ||||||||   || || |||||||     |||   |  || ||||
Db       485 ACCACCTAGAGCCTTGGATCCAGGACAACGGCGGCTGGGACACTTTCGTGGAACTCTACG 544

Qy       455 GGGACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGA 514
            | ||   ||   |  |||   |||       | |||| |   |       |   |   ||
Db       545 GAAACAATGCAGCAGCTGAGAGCCGGAAAGGCCAGGAGCGCTTCAACCGCTGGTTCCTGA 604

Qy       515 CAGTGCTGACGGGGGCCG 532
            | |   |||| | ||| |
Db       605 CGGGCATGACTGTGGCTG 622


Search completed: April 10, 2005, 22:38:32
Job time : 502.358 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 14:47:25 ; Search time 2841.37 Seconds
(without alignments)
7810.120 Million cell updates/sec

Title: US-09-925-674B-6
Perfect score: 583
Sequence: 1 atggcgaccccagcctcggc.....ctttttgctagcaagtgaa 583

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	573.4	98.4	727	6	CD617893	CD617893 56057475J
	2	572.4	98.2	582	9	AY421020	AY421020 Homo sapi
c	3	571.8	98.1	629	6	CD617891	CD617891 56057367J
	4	550	94.3	804	1	AL157542	AL157542 DKFZp761D
	5	548.4	94.1	1030	2	BE793530	BE793530 601590016
	6	526.4	90.3	643	7	CN281020	CN281020 170005318
	7	522.8	89.7	582	9	AY421022	AY421022 Mus muscu
	8	522.8	89.7	1949	3	AK015644	AK015644 Mus muscu
	9	522.8	89.7	3487	3	AK004680	AK004680 Mus muscu
	10	521.2	89.4	969	6	BY715200	BY715200 BY715200
	11	518.2	88.9	662	6	CD617892	CD617892 56057475H
	12	500	85.8	627	6	CD617890	CD617890 56057367H
	13	483.4	82.9	697	4	BI770566	BI770566 603060362
	14	465.6	79.9	967	5	BU503850	BU503850 AGENCOURT
	15	448	76.8	516	7	CN281015	CN281015 170005321
	16	443	76.0	626	6	CA391923	CA391923 cs20c09.y
	17	436	74.8	757	7	CK359685	CK359685 AGENCOURT
	18	434.2	74.5	713	5	BP753931	BP753931 BP753931
	19	423.2	72.6	583	5	BP355256	BP355256 BP355256
	20	423	72.6	583	5	BP249141	BP249141 BP249141
	21	421.4	72.3	584	5	BP311709	BP311709 BP311709
	22	417.6	71.6	643	4	BI910270	BI910270 603069493
	23	417	71.5	583	5	BP202031	BP202031 BP202031
	24	397	68.1	815	2	BF785386	BF785386 602111728
	25	381.8	65.5	623	6	CB578463	CB578463 AMGNNUC:N
	26	375.4	64.4	854	3	AK013244	AK013244 Mus muscu
	27	364.2	62.5	792	4	BG298789	BG298789 602396527
	28	360	61.7	548	6	CA407899	CA407899 1004048 H
	29	359	61.6	869	5	BU557268	BU557268 AGENCOURT
	30	359	61.6	872	5	BU557410	BU557410 AGENCOURT
	31	357.2	61.3	540	2	AW258810	AW258810 um74a02.y
	32	347.2	59.6	507	7	CN281011	CN281011 328742965
	33	346.6	59.5	582	5	BP216712	BP216712 BP216712
	34	340.2	58.4	752	7	CO401477	CO401477 AGENCOURT
	35	332	56.9	437	6	CB790932	CB790932 AMGNNUC:N
	36	331.2	56.8	440	6	CB749817	CB749817 AMGNNUC:M
c	37	330.8	56.7	630	7	CO040065	CO040065 UI-M-BH1-
	38	326.8	56.1	758	4	BI764428	BI764428 603050701
	39	317.8	54.5	1053	5	BU931540	BU931540 AGENCOURT
	40	311.2	53.4	327	9	AY421021	AY421021 Pan trogl
	41	305.2	52.3	559	6	BY704881	BY704881 BY704881
	42	297.8	51.1	548	7	CF533813	CF533813 UI-M-FY0-
	43	294.2	50.5	749	4	BG677345	BG677345 602624059
	44	293.8	50.4	645	6	BY740551	BY740551 BY740551
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ALIGNMENTS

RESULT 1
CD617893/c
LOCUS CD617893 727 bp mRNA linear EST 12-JAN-2004
DEFINITION 56057475J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD617893
VERSION CD617893.1 GI:40266158
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 727)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES Location/Qualifiers
source 1. .727
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
ORIGIN

Query Match 98.4%; Score 573.4; DB 6; Length 727;
Best Local Similarity 99.0%; Pred. No. 2e-132;
Matches 577; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Db        608 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 549

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 489

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Db        488 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 429

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        428 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 369

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Db        368 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 309

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Db        308 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 249

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420

Db        248 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 189

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Db        188 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 129

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Db        128 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 69

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 583

Db         68 GGGGCACTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 26
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LOCUS       AY421020                582 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Homo sapiens BCL2L2 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY421020
VERSION     AY421020.1  GI:39776977
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 582)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence as made by sequencing genomic exons and ordering them
            based on alignment.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
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                     /gene="BCL2L2"
                     /locus_tag="HCM7418"
ORIGIN

  Query Match             98.2%;  Score 572.4;  DB 9;  Length 582;
  Best Local Similarity   99.0%;  Pred. No. 3.5e-132;
  Matches  576;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;
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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Db        121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

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Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420

Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582

Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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RESULT 3
CD617891/c
LOCUS       CD617891                629 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  56057367J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD617891
VERSION     CD617891.1  GI:40266156
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 629)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .629
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                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match             98.1%;  Score 571.8;  DB 6;  Length 629;
  Best Local Similarity   98.8%;  Pred. No. 4.9e-132;
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Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Db        547 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 488

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Db        487 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 428

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Db        367 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 308

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Db        307 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 248

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Db        247 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 188

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 583
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Db         67 GGGGCCTCGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 25


RESULT 4
AL157542
LOCUS       AL157542                804 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp761D0816_r1 761 (synonym: hamy2) Homo sapiens cDNA clone
            DKFZp761D0816 5', mRNA sequence.
ACCESSION   AL157542
VERSION     AL157542.1  GI:7057943
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 804)
  AUTHORS   Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.
  TITLE     EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp761D0816) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:9606"
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                      /tissue_type="amygdala"
                      /dev_stage="adult"
                      /lab_host="DH10B"
                      /clone_lib="761 (synonym: hamy2)"
                      /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
ORIGIN

  Query Match             94.3%;  Score 550;  DB 1;  Length 804;
  Best Local Similarity   98.6%;  Pred. No. 1.4e-126;
  Matches  575;  Conservative    0;  Mismatches    6;  Indels    2;  Gaps    2;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Db        194 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 253

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 313

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        314 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 373

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Db        434 GTCTTTGGGGCTGCACTGTGTGCNGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 493

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        494 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 553

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Db        554 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGAC-GGGCCCTGGAGGAGGCGCGG 612

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 583
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Db        672 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 714


RESULT 5
BE793530
LOCUS       BE793530                1030 bp    mRNA    linear   EST 20-SEP-2000
DEFINITION  601590016F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944307 5',
            mRNA sequence.
ACCESSION   BE793530
VERSION     BE793530.1  GI:10214832
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1030)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
```

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COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM800  row: p  column: 04
            High quality sequence start: 5
            High quality sequence stop: 709.
FEATURES                Location/Qualifiers
     source             1. .1030
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:3944307"
                        /tissue_type="small cell carcinoma"
                        /cell_line="MGC3"
                        /lab_host="DH10B (phage-resistant)"
                        /clone_lib="NIH_MGC_7"
                        /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                        EcoRI; cDNA made by oligo-dT priming.  Directionally
                        cloned into EcoRI/XhoI sites using the following 5'
                        adaptor: GGCACGAG(G).  Size-selected >500bp for average
                        insert size 1.8kb.  Library constructed by Ling Hong in
                        the laboratory of Gerald M. Rubin (University of
                        California, Berkeley) using  ZAP-cDNA synthesis kit
                        (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

  Query Match             94.1%;  Score 548.4;  DB 2;  Length 1030;
  Best Local Similarity   96.4%;  Pred. No. 3.7e-126;
  Matches  561;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 203

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 263

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 323

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        324 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 383

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        384 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 443

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 503

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        504 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 563

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 623

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
              |||||||||| ||| |||||||||||||||||||||||||||||| ||||||||||||||
Db        624 CGTCTGCGGGGAGGGGACTGGGCATCAGTGAGGACAGTGCTGACGGGGGGCGTGGCACTG 683

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
              |||| |||||  |      ||| | ||||||||||||||||||
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Db        684 GGGGGCCTGGGTAACTGTAGGGGCCTTTTTGCTAGCAAGTGA 725


RESULT 6
CN281020
LOCUS       CN281020                643 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000531876837 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN281020
VERSION     CN281020.1  GI:47297434
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 643    Std Error: 0.00.
FEATURES                Location/Qualifiers
     source             1. .643
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /tissue_type="embryonic stem cells, embryoid bodies
                        derived from H1, H7 and H9 cells"
                        /clone_lib="GRN_EB"
                        /note="oligo dT primed, full-length enriched cDNA library
                        from embryoid body outgrowths derived from hES cell lines
                        H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                        conditions."
ORIGIN

  Query Match             90.3%;  Score 526.4;  DB 7;  Length 643;
  Best Local Similarity   98.9%;  Pred. No. 1.1e-120;
  Matches  530;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 167

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 227

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 287

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        288 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 347

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        348 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 407

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Db        408 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 467

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
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Db        468 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 527

Qy        421 AGTGGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Db        528 AGTGGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 587

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGC 536
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        588 CGTCTGCGGGAGGGGAACTGGGCATCATTGAGGACAGTGCTGACGGGGGCCGTGGC 643
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RESULT 7
AY421022

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LOCUS       AY421022                582 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Mus musculus BCL2L2 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY421022
VERSION     AY421022.1  GI:39776979
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 582)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence as made by sequencing genomic exons and ordering them
            based on alignment.
FEATURES             Location/Qualifiers
     source          1. .582
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>582
                     /gene="BCL2L2"
                     /locus_tag="HCM7418"
ORIGIN
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  Query Match             89.7%;  Score 522.8;  DB 9;  Length 582;
  Best Local Similarity   93.6%;  Pred. No. 8.5e-120;
  Matches  545;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
              |||||||||||||||  ||||||||||||||||||| ||||| |||||||||||| |||
Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
              |||||||||||||||||||||||||||||||||||||| ||||| |||||||| || |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
              |||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
              |||||  |||||||||||||| |||||||||| |||||||||| ||||| || ||||||
Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||||||||| || ||||| ||  ||||||||
Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
              |||||||||||  |||||||||||||||||||||||| || ||||  |||||||||||||||
Db        361 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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RESULT 8
AK015644

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LOCUS       AK015644                1949 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male testis cDNA, RIKEN full-length enriched
            library, clone:4930488D08 product:Bcl2-like 2, full insert
            sequence.
ACCESSION   AK015644
VERSION     AK015644.1  GI:12854052
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
        :   Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
```

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            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1949)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
            Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
            Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
            Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
            Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
            Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.jp/) for further
            details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCC 3']. cDNA was cleaved
            with BamHI and XhoI. cDNA of size comprised longer than 7 kb was
            selected before cloning. Vector: a modified pBluescript KS(+) after
            bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
            end: BamHI. Host: DH10B.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:4930488D08"
                     /db_xref="taxon:10090"
                     /clone="4930488D08"
                     /sex="male"
                     /tissue_type="testis"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
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                     /note="unnamed protein product; Bcl2-like 2
                     (MGD|MGI:108052)
                     putative"
                     /codon_start=1
                     /protein_id="BAB29912.1"
                     /db_xref="GI:12854053"
                     /translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
                     AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
                     GAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
                     RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
ORIGIN

  Query Match             89.7%;  Score 522.8;  DB 3;  Length 1949;
  Best Local Similarity   93.6%;  Pred. No. 1e-119;
  Matches  545;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy         1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
             |||||||||||||||||  ||||||||||||||||||| ||||| ||||||||||| |||
Db       132 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 191

Qy        61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
             |||||||||||||||||||||||||||||||||||||| ||||| |||||||| || |||
Db       192 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 251

Qy       121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
             ||||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db       252 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 311

Qy       181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
             |||||||| ||||| |||||||| || |||||||||||||||||||||||||||||||||
Db       312 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 371

Qy       241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
             ||||| |||||||||||||| ||||||||||| ||||||||||| ||||| || ||||||
Db       372 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 431

Qy       301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
              ||||||||||||| ||||||||||||||||||||||| || ||||| ||  ||||||||
Db       432 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 491

Qy       361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
             ||||||||||| ||||||||||||||||||||||| || ||||  |||||||||||||||
Db       492 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 551

Qy       421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Db       552 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 611

Qy       481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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RESULT 9
AK004680
LOCUS       AK004680                3487 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male lung cDNA, RIKEN full-length enriched
            library, clone:1200009L24 product:Bcl2-like 2, full insert
            sequence.
ACCESSION   AK004680
VERSION     AK004680.1  GI:12836027
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
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  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3487)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
            Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
            Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
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            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
            Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
            Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.jp/) for further
            details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence[5'
            GAGAGAGAGAAGGATCCAAGAGCTCAATTAATTTAATTAAACCCCCCCCCCC 3']. cDNA was
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                     /sex="male"
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                     (MGD|MGI:108052)
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                     /protein_id="BAB23468.1"
                     /db_xref="GI:12836028"
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ORIGIN

  Query Match             89.7%;  Score 522.8;  DB 3;  Length 3487;
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Db        209 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 268

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Db        269 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 328

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Db        449 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 508

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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RESULT 10
BY715200
LOCUS       BY715200                969 bp    mRNA    linear   EST 17-DEC-2002
DEFINITION  BY715200 RIKEN full-length enriched, adult male testis Mus musculus
            cDNA clone 4930488D08 5', mRNA sequence.
ACCESSION   BY715200
VERSION     BY715200.1  GI:27128317
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 969)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
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Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers

source 1. .969
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/note="Site_1: XhoI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAGCGGCCGCAATTAATTCTCGAGTTAATTAAATTAATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. "

ORIGIN

Query Match 89.4%; Score 521.2; DB 6; Length 969;
Best Local Similarity 93.5%; Pred. No. 2.3e-119;
Matches 544; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Db        552 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 611

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Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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Db        672 GGGGCTCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 713
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RESULT 11
CD617892
LOCUS CD617892 662 bp mRNA linear EST 12-JAN-2004
DEFINITION 56057475H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD617892
VERSION CD617892.1 GI:40266157
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 662)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK

Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES Location/Qualifiers
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/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 88.9%; Score 518.2; DB 6; Length 662;
Best Local Similarity 98.3%; Pred. No. 1.2e-118;
Matches 534; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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Qy        361 CAAGTGCAGGAGTGGA-TGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAG 419
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Db        600 GCGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCCTG 659

Qy        540 GGG 542
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Db        660 GGG 662
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RESULT 12
CD617890
LOCUS CD617890 627 bp mRNA linear EST 12-JAN-2004
DEFINITION 56057367H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD617890
VERSION CD617890.1 GI:40266155
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 627)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES Location/Qualifiers
source 1. .627
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 85.8%; Score 500; DB 6; Length 627;
Best Local Similarity 99.0%; Pred. No. 4.2e-114;
Matches 503; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Db        120 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 179

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Db        180 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 239

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Db        240 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 299

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480
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Db        540 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 599

Qy        481 CGTCTGCGGGAGGGGAACTGGGCATCAG 508
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Db        600 CGTCTGCGGGAGGGGAACTGGGCATCAG 627
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RESULT 13
BI770566
LOCUS BI770566 697 bp mRNA linear EST 25-SEP-2001
DEFINITION 603060362F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209862 5',
mRNA sequence.
ACCESSION BI770566
VERSION BI770566.1 GI:15762144
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 697)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

```
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11526  row: k  column: 15
            High quality sequence start: 21
            High quality sequence stop: 695.
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                        anonymous pool of 24 week female lung, 16 week female
                        spleen, and 20-22 week male spleens.  Library is oligo-dT
                        primed and directionally cloned (EcoRV site is destroyed
                        upon  cloning).  Average insert size 1.4 kb, insert size
                        range 1-3 kb. Library is normalized and enriched for
                        full-length clones and was  constructed by C. Gruber
                        (Invitrogen).  Research Genetics tracking  code 026. Note:
                        this is a NIH_MGC Library."
ORIGIN

  Query Match             82.9%;  Score 483.4;  DB 4;  Length 697;
  Best Local Similarity   98.0%;  Pred. No. 6e-110;
  Matches  542;  Conservative     0;  Mismatches    6;  Indels    5;  Gaps    5;

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Db        145 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 204

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Db        205 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 264

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Db        265 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 324

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        325 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 384

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Db        385 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 444

Qy        301 CTCTTTGGGGCTGCACTGTG-TGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGG 359
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Db        445 GTCTTTGGGGCTGCACTGTGTTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGG 504

Qy        360 ACAAGTGCAGGAGTGGATGGTGGCCTACCT-GGAGACGCGGCTGGTCGACTGGATCCACA 418
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Db        505 ACAAGTGCAGGAGTGGATGGTGGCCTACCTGGGAGACGCGGCTGGCTGACTGGATCCACA 564

Qy        419 GCAGTGGGGGCTGGGCGGAGTTCACAGCTCTATAC-GGGGACGGGGCCCTGGAGGAGGCG 477
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Db        565 GCAGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGGACGGGGCCCTGGAGGAGGCG 624

Qy        478 CGGCGTCTGCGGGAGGGGAACTGGGCA-TCAGTGAGGACAG-TGCTGACGGGGGCCGTGG 535
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Db        625 CGGCGTCTGCGGGAGGGGAACTGGGCACTCAGTGAGGACAGTTGCTGACGGGAGCCGTGG 684

Qy        536 CACTGGGGGCCCT 548
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Db        685 CACTGGGGGCCCT 697


RESULT 14
BU503850
LOCUS       BU503850                 967 bp    mRNA    linear   EST 12-SEP-2002
DEFINITION  AGENCOURT_10030867 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6491566
            5', mRNA sequence.
ACCESSION   BU503850
VERSION     BU503850.1  GI:22810083
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 967)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14043  row: c  column: 23
            High quality sequence stop: 524.
FEATURES                Location/Qualifiers
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                        /clone="IMAGE:6491566"
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                        /lab_host="DH10B (phage-resistant)"
                        /clone_lib="NIH_MGC_94"
                        /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                        Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                        Average insert size 3.3 kb. Library enriched for
                        full-length clones and constructed by Life Technologies.
                        Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             79.9%;  Score 465.6;  DB 5;  Length 967;
  Best Local Similarity   92.5%;  Pred. No. 1.8e-105;
  Matches  544;  Conservative     0;  Mismatches   39;  Indels    5;  Gaps    5;

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Db        130 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 189

Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Db        190 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 249

Qy        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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Db        250 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 309

Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        310 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 369

Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Db        370 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 429

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Db        490 CAAGTGCAGGATTGGATGGTGGCCTACCCTGGAGACACGTCTGGCTGACTGGATCCACAG 549

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Db        550 CAGTGGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGGCCCTGGAGGAGGCA 609

Qy        478 CGGCGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGAC-GGGGGCCGTGGC 536
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DEFINITION 17000532179318 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN281015
VERSION CN281015.1 GI:47297429
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 516)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 516 Std Error: 0.00.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."
ORIGIN

Query Match 76.8%; Score 448; DB 7; Length 516;
Best Local Similarity 98.9%; Pred. No. 4e-101;
Matches 451; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Qy         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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Qy        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Db        301 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 360

Qy        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Db        361 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 420

Qy        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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Db        421 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 480

Qy        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGG 456
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 10, 2005, 22:21:58 ; Search time 19.5 Seconds
(without alignments)
738.834 Million cell updates/sec

Title: US-09-925-674B-7
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Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	1002	99.5	193	1	US-08-798-897-4	Sequence 4, Appli
4	1002	99.5	193	2	US-08-978-523-4	Sequence 4, Appli
5	1000	99.3	193	4	US-09-155-327G-9	Sequence 9, Appli
6	997	99.0	192	1	US-08-798-897-6	Sequence 6, Appli
7	997	99.0	192	2	US-08-978-523-6	Sequence 6, Appli
8	996	98.9	193	1	US-08-798-897-3	Sequence 3, Appli
9	996	98.9	193	2	US-08-978-523-3	Sequence 3, Appli
10	991	98.4	192	1	US-08-798-897-5	Sequence 5, Appli
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13	766	76.1	365	4	US-09-149-476-696	Sequence 696, App
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15	433.5	43.0	411	4	US-09-639-245-2	Sequence 2, Appli
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28	428.5	42.6	233	4	US-08-470-865-14	Sequence 14, Appl
29	428.5	42.6	233	4	US-09-155-327G-12	Sequence 12, Appl
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31	428.5	42.6	233	5	PCT-US95-04600-24	Sequence 24, Appl
32	425	42.2	225	3	US-09-101-519-1	Sequence 1, Appli
33	423.5	42.1	233	1	US-08-607-269-23	Sequence 23, Appl
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35	413	41.0	236	1	US-08-607-269-22	Sequence 22, Appl
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40	412.5	41.0	239	2	US-08-337-646A-10	Sequence 10, Appl
41	412.5	41.0	239	2	US-08-856-531-10	Sequence 10, Appl
42	412.5	41.0	239	2	US-08-856-034-10	Sequence 10, Appl
43	412.5	41.0	239	3	US-09-127-048-8	Sequence 8, Appli
44	412.5	41.0	239	3	US-08-927-326-10	Sequence 10, Appl
45	412.5	41.0	239	4	US-09-379-820A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-155-327G-7
; Sequence 7, Application US/09155327G
; Patent No. 6790637
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 2096584
; CURRENT APPLICATION NUMBER: US/09/155,327G
; CURRENT FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 193
; TYPE: PRT
; ORGANISM: HUMAN
US-09-155-327G-7

Query Match 100.0%; Score 1007; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193
```

RESULT 2
US-09-949-016-10928
; Sequence 10928, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

```
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10928
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10928

  Query Match             100.0%;  Score 1007;  DB 4;  Length 193;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-107;
  Matches  193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 3
US-08-798-897-4
; Sequence 4, Application US/08798897
; Patent No. 5789201
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  193 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-798-897-4

  Query Match             99.5%;  Score 1002;  DB 1;  Length 193;
  Best Local Similarity   99.5%;  Pred. No. 1.2e-106;
  Matches  192;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 4
US-08-978-523-4
; Sequence 4, Application US/08978523
; Patent No. 5883229
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,523
;      FILING DATE:  herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  193 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-978-523-4

  Query Match             99.5%;  Score 1002;  DB 2;  Length 193;
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  Best Local Similarity   99.5%;  Pred. No. 1.2e-106;
  Matches  192;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 5
US-09-155-327G-9
; Sequence 9, Application US/09155327G
; Patent No. 6790637
; GENERAL INFORMATION:
;  APPLICANT: AMRAD Operations Pty Ltd
;  TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
;  TITLE OF INVENTION:  FAMILY OF APOPTOSIS-CONTROLLING GENES
;  FILE REFERENCE: 2096584
;  CURRENT APPLICATION NUMBER: US/09/155,327G
;  CURRENT FILING DATE:  1999-03-29
;  PRIOR APPLICATION NUMBER: PN8965
;  PRIOR FILING DATE: 1996-03-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-155-327G-9

  Query Match             99.3%;  Score 1000;  DB 4;  Length 193;
  Best Local Similarity   99.0%;  Pred. No. 2e-106;
  Matches  191;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 6
US-08-798-897-6
; Sequence 6, Application US/08798897
; Patent No. 5789201
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  192 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-798-897-6

  Query Match             99.0%;  Score 997;  DB 1;  Length 192;
  Best Local Similarity   99.5%;  Pred. No. 4.3e-106;
  Matches  191;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60

Qy         62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120

Qy        122 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

Qy        182 ALVTVGAFFASK 193
              ||||||||||||
Db        181 ALVTVGAFFASK 192


RESULT 7
US-08-978-523-6
; Sequence 6, Application US/08978523
; Patent No. 5883229
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  US/08/978,523
;       FILING DATE:  herewith
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/798,897
;       FILING DATE:  February 11, 1997
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Esmond, Robert W.
;       REGISTRATION NUMBER:  32,893
;       REFERENCE/DOCKET NUMBER:  1483.0140002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  192 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-978-523-6

  Query Match             99.0%;  Score 997;  DB 2;  Length 192;
  Best Local Similarity   99.5%;  Pred. No. 4.3e-106;
  Matches  191;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60

Qy         62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120

Qy        122 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

Qy        182 ALVTVGAFFASK 193
              ||||||||||||
Db        181 ALVTVGAFFASK 192


RESULT 8
US-08-798-897-3
; Sequence 3, Application US/08798897
; Patent No. 5789201
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  193 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-798-897-3

  Query Match             98.9%;  Score 996;  DB 1;  Length 193;
  Best Local Similarity   98.4%;  Pred. No. 5.7e-106;
  Matches  190;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 9
US-08-978-523-3
; Sequence 3, Application US/08978523
; Patent No. 5883229
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,523
;      FILING DATE:  herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  193 amino acids
;      TYPE:  amino acid
```

```
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-978-523-3

  Query Match             98.9%;  Score 996;  DB 2;  Length 193;
  Best Local Similarity   98.4%;  Pred. No. 5.7e-106;
  Matches  190;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 10
US-08-798-897-5
; Sequence 5, Application US/08798897
; Patent No. 5789201
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  192 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-798-897-5

  Query Match             98.4%;  Score 991;  DB 1;  Length 192;
  Best Local Similarity   98.4%;  Pred. No. 2.1e-105;
  Matches  189;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60

Qy         62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120

Qy        122 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
              ||:||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

Qy        182 ALVTVGAFFASK 193
              ||||||||||||
Db        181 ALVTVGAFFASK 192


RESULT 11
US-08-978-523-5
; Sequence 5, Application US/08978523
; Patent No. 5883229
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,523
;      FILING DATE:  herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  192 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-978-523-5

  Query Match             98.4%;  Score 991;  DB 2;  Length 192;
  Best Local Similarity   98.4%;  Pred. No. 2.1e-105;
  Matches  189;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60

Qy         62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120

Qy        122 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
              ||:||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

Qy        182 ALVTVGAFFASK 193
              ||||||||||||
Db        181 ALVTVGAFFASK 192
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Db        121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

Qy        182 ALVTVGAFFASK 193
              ||||||||||||
Db        181 ALVTVGAFFASK 192


RESULT 12
US-09-155-327G-10
; Sequence 10, Application US/09155327G
; Patent No. 6790637
; GENERAL INFORMATION:
;  APPLICANT: AMRAD Operations Pty Ltd
;  TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
;  TITLE OF INVENTION:  FAMILY OF APOPTOSIS-CONTROLLING GENES
;  FILE REFERENCE: 2096584
;  CURRENT APPLICATION NUMBER: US/09/155,327G
;  CURRENT FILING DATE:  1999-03-29
;  PRIOR APPLICATION NUMBER: PN8965
;  PRIOR FILING DATE: 1996-03-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 333
;   TYPE: PRT
;   ORGANISM: murine
US-09-155-327G-10

  Query Match           76.2%;  Score 767;  DB 4;  Length 333;
  Best Local Similarity  74.4%;  Pred. No. 2.2e-79;
  Matches  157;  Conservative    6;  Mismatches   18;  Indels   30;  Gaps    4;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYG--DGALEEARRLRE-------------- 164
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Db        121 QVQDWMVAYLETRLADWIHSSGGW-ELEAIKARVREMEEEAEKLKELQNEVEKQMNMSPP 179

Qy        165 -GN------------WASVRTVLTGAVALGA 182
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Db        180 PGNAGPVIMSLEEKMEADARSIYVGNVDYGA 210


RESULT 13
US-09-149-476-696
; Sequence 696, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P1
;  CURRENT APPLICATION NUMBER: US/09/149,476
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: PCT/US98/04493
;  EARLIER FILING DATE: 1998-03-06
;  EARLIER APPLICATION NUMBER: 60/040,162
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,333
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/038,621
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,626
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,334
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,336
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,163
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/047,600
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,615
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,597
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,502
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,633
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,583
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,617
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,618
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,503
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,592
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,581
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,584
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,500
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,587
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,492
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,598
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,613
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,582
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,596
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,612
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,632
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,601
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/043,580
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,568
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,314
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,569
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,311
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,671
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,674
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,669
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,312
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,313
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,672
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,315
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/048,974
;  EARLIER FILING DATE: 1997-06-06
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; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 76.1%; Score 766; DB 4; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.3e-79;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGW 144
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Db        121 QVQEWMVAYLETRLADWIHSSGGW 144
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RESULT 14
US-09-010-147B-24
; Sequence 24, Application US/09010147B
; Patent No. 6653445
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Human Proteins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/010,147B
; FILING DATE: 12-No. 6653445-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,205
; FILING DATE: 21-JAN-1997
; APPLICATION NUMBER: US 60/034,204
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jonathan L. Klein
; REGISTRATION NUMBER: 41,119
; REFERENCE/DOCKET NUMBER: PF353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-010-147B-24

Query Match 76.1%; Score 766; DB 4; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.3e-79;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGW 144
              ||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGW 144
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RESULT 15
US-09-639-245-2
; Sequence 2, Application US/09639245
; Patent No. 6737511
; GENERAL INFORMATION:
; APPLICANT: Youle et al.
; TITLE OF INVENTION: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL
; TITLE OF INVENTION: FUSION PROTEIN INHIBITS APOPTOSIS
; FILE REFERENCE: 4239-55417
; CURRENT APPLICATION NUMBER: US/09/639,245
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/149,220
; PRIOR FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: genetic fusion
US-09-639-245-2

Query Match 43.0%; Score 433.5; DB 4; Length 411;
Best Local Similarity 39.9%; Pred. No. 5.2e-41;
Matches 93; Conservative 26; Mismatches 63; Indels 51; Gaps 4;

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Qy         11 RALVADFVGYKLRQKGY----------------------------VCGAGP----GEGPAA 39
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Db         26 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 85

Qy         40 D------------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
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Db         86 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 145

Qy         82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
              | :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |_ ||  :
Db        146 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQEN 205

Qy        142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGALVTVGAFFAS 192
              |||  |  |||: |  |:|: :|    |       : | | ||:| :  |: |:
Db        206 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRKAYSAA 258
```

Search completed: April 10, 2005, 22:45:27
Job time : 21.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 10, 2005, 20:17:32 ; Search time 59 Seconds
(without alignments)
1675.106 Million cell updates/sec

Title: US-09-925-674B-7
Perfect score: 1007
Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1007	100.0	193	1	BCLW_HUMAN	Q92843 homo sapien
2	1000	99.3	193	1	BCLW_MOUSE	P70345 mus musculu
3	996	98.9	193	2	O88996	O88996 rattus norv
4	996	98.9	219	2	Q7TS60	Q7ts60 rattus norv
5	987	98.0	192	2	Q6A093	Q6a093 mus musculu
6	951	94.4	193	2	Q8CGL4	Q8cgl4 mus musculu
7	761	75.6	178	2	Q8CFR2	Q8cfr2 mus musculu
8	761	75.6	178	2	Q9CYW5	Q9cyw5 mus musculu
9	651.5	64.7	188	2	Q6GP82	Q6gp82 xenopus lae
10	646.5	64.2	228	1	AR1_XENLA	Q91827 xenopus lae
11	440.5	43.7	233	2	Q9MYW4	Q9myw4 oryctolagus
12	433.5	43.0	233	2	Q8SQ42	Q8sq42 felis silve
13	432.5	42.9	229	1	BCLX_CHICK	Q07816 gallus gall
14	431.5	42.9	233	1	BCLX_PIG	O77737 sus scrofa
15	431.5	42.9	233	2	Q9N1A2	Q9n1a2 sus scrofa
16	428.5	42.6	233	1	BCLX_HUMAN	Q07817 homo sapien
17	428.5	42.6	233	1	BCLX_MOUSE	Q64373 mus musculu
18	428.5	42.6	233	1	BCLX_RAT	P53563 rattus norv
19	428.5	42.6	233	2	Q76LT7	Q76lt7 canis famil
20	428.5	42.6	233	2	Q9MZS7	Q9mzs7 ovis aries
21	423.5	42.1	233	1	BCL2_CHICK	Q00709 gallus gall
22	416.5	41.4	229	1	BCL2_BOVIN	O02718 bos taurus
23	414	41.1	236	1	BCL2_RAT	P49950 rattus norv
24	413	41.0	236	1	BCL2_MOUSE	P10417 mus musculu
25	413	41.0	236	2	Q7TSN8	Q7tsn8 rattus norv
26	413	41.0	236	2	Q8BQK4	Q8bqk4 mus musculu
27	412.5	41.0	239	1	BCL2_HUMAN	P10415 homo sapien
28	403	40.0	236	1	BCL2_CRILO	Q9jjv8 cricetulus
29	403	40.0	238	2	Q90Z98	Q90z98 brachydanio
30	402.5	40.0	239	2	Q75SV7	Q75sv7 canis famil
31	402	39.9	79	2	Q7TS61	Q7ts61 rattus norv
32	401	39.8	180	2	Q9BDD5	Q9bdd5 bos taurus
33	401	39.8	217	2	Q99N35	Q99n35 mus musculu
34	399	39.6	236	2	Q923R6	Q923r6 cricetulus
35	398.5	39.6	180	2	Q9BDX7	Q9bdx7 bos taurus
36	398.5	39.6	201	2	Q6GLI5	Q6gli5 xenopus tro
37	396.5	39.4	235	2	Q8I008	Q8i008 felis silve
38	396	39.3	236	2	Q6R755	Q6r755 canis famil
39	380.5	37.8	284	2	Q7TS62	Q7ts62 rattus norv
40	374.5	37.2	188	2	Q9QWX2	Q9qwx2 mus musculu
41	374.5	37.2	235	2	O35843	O35843 mus musculu
42	373.5	37.1	188	2	Q9H1R6	Q9h1r6 homo sapien
43	373	37.0	204	2	Q90ZH2	Q90zh2 xenopus lae
44	371	36.8	204	1	AR11_XENLA	Q91828 xenopus lae
45	366.5	36.4	153	2	Q7YRB6	Q7yrb6 canis famil

ALIGNMENTS

RESULT 1
BCLW_HUMAN
ID BCLW_HUMAN STANDARD; PRT; 193 AA.
AC Q92843;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Apoptosis regulator Bcl-W (Bcl-2-like 2 protein).
GN Name=BCL2L2; Synonyms=BCLW, KIAA0271;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL Oncogene 13:665-675(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.";
RL DNA Res. 3:321-329(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```
CC   -!- FUNCTION: Promotes cell survival.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC       in a wide range of tissues, with highest levels in brain, colon,
CC       and salivary gland.
CC   -!- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC       function.
CC   -!- SIMILARITY: Belongs to the Bcl-2 family.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U59747; AAB09055.1; -.
DR   EMBL; D87461; BAA19666.2; ALT_INIT.
DR   EMBL; BC021198; AAH21198.1; -.
DR   PDB; 1MK3; NMR; A=2-172.
DR   PDB; 1O0L; NMR; A=1-183.
DR   Genew; HGNC:995; BCL2L2.
DR   H-InvDB; HIX0011536; -.
DR   MIM; 601931; -.
DR   GO; GO:0005737; C:cytoplasm; NAS.
DR   GO; GO:0006916; P:anti-apoptosis; TAS.
DR   GO; GO:0007283; P:spermatogenesis; TAS.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   3D-structure; Apoptosis.
FT   DOMAIN        9     29       BH4.
FT   DOMAIN       85    104       BH1.
FT   DOMAIN      136    151       BH2.
SQ   SEQUENCE   193 AA;  20774 MW;  3792243A50281761 CRC64;

  Query Match             100.0%;  Score 1007;  DB 1;  Length 193;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-82;
  Matches  193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 2
BCLW_MOUSE
ID   BCLW_MOUSE     STANDARD;      PRT;   193 AA.
AC   P70345;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Apoptosis regulator Bcl-W (Bcl-2-like 2 protein).
GN   Name=Bcl2l2; Synonyms=Bclw;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96358615; PubMed=8761287;
RA   Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
RA   Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT   "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL   Oncogene 13:665-675(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/10J;
RX   MEDLINE=98160183; PubMed=9500547;
RA   Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,
RA   Russell L.D., Macgregor G.R.;
RT   "Testicular degeneration in Bclw-deficient mice.";
RL   Nat. Genet. 18:251-256(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
CC   -!- FUNCTION: Promotes cell survival.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC       in a wide range of tissues, with highest levels in brain, colon,
CC       and salivary gland.
CC   -!- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC       function.
CC   -!- SIMILARITY: Belongs to the Bcl-2 family.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U59746; AAB09056.1; -.
DR   EMBL; AF030769; AAB86430.1; -.
DR   EMBL; AK015644; BAB29912.1; -.
DR   HSSP; Q92843; 1O0L.
DR   MGD; MGI:108052; Bcl2l2.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006915; P:apoptosis; IDA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis.
FT   DOMAIN        9     29       BH4.
FT   DOMAIN       85    104       BH1.
FT   DOMAIN      136    151       BH2.
SQ   SEQUENCE   193 AA;  20790 MW;  36CA185F5945DFB4 CRC64;

  Query Match             99.3%;  Score 1000;  DB 1;  Length 193;
  Best Local Similarity   99.0%;  Pred. No. 1.8e-81;
  Matches  191;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
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Db        181 GALVTVGAFFASK 193


RESULT 3
O88996
ID   O88996      PRELIMINARY;      PRT;   193 AA.
AC   O88996;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Bcl-w (Hypothetical protein).
GN   Name=bcl-w;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=99292146; PubMed=10366024; DOI=10.1016/S0306-4522(98)00642-3;
RA   Hamner S., Skoglosa Y., Lindholm D.;
RT   "Differential expression of bcl-w and bcl-x messenger RNA in the
RT   developing and adult rat nervous system.";
RL   Neuroscience 91:673-684(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=22672518; PubMed=12787069;
RA   Itoh T., Itoh A., Pleasure D.;
RT   "Bcl-2-related protein family gene expression during oligodendroglial
RT   differentiation.";
RL   J. Neurochem. 85:1500-1512(2003).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF096291; AAC64200.1; -.
DR   EMBL; AY185098; AAO64468.1; -.
DR   EMBL; BC074021; AAH74021.1; -.
DR   HSSP; Q92843; 1O0L.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   193 AA;  20820 MW;  36D6742F4529AFB4 CRC64;

  Query Match             98.9%;  Score 996;  DB 2;  Length 193;
  Best Local Similarity   98.4%;  Pred. No. 4.1e-81;
  Matches  190;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193
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RESULT 4
Q7TS60
ID   Q7TS60       PRELIMINARY;      PRT;   219 AA.
AC   Q7TS60;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   BCL-WEL.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=22672518; PubMed=12787069;
RA   Itoh T., Itoh A., Pleasure D.;
RT   "Bcl-2-related protein family gene expression during oligodendroglial
RT   differentiation.";
RL   J. Neurochem. 85:1500-1512(2003).
DR   EMBL; AY185100; AAO64470.1; -.
DR   HSSP; Q07817; 1R2D.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   219 AA;  23720 MW;  30E36041BC1DC66F CRC64;

  Query Match           98.9%;  Score 996;  DB 2;  Length 219;
  Best Local Similarity  98.4%;  Pred. No. 4.8e-81;
  Matches  190;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 86

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 146

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 206

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        207 GALVTVGAFFASK 219


RESULT 5
Q6A093
ID   Q6A093       PRELIMINARY;      PRT;   192 AA.
AC   Q6A093;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   MKIAA0271 protein (Fragment).
GN   Name=mKIAA0271;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA   Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA   Nagase T., Ohara O., Koga H.;
RT   "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT   IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
RT   cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT   Randomly Sampled from Size-Fractionated Libraries.";
RL   DNA Res. 11:205-218(2004).
DR   EMBL; AK172925; BAD32203.1; -.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006915; P:apoptosis; IDA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   192 AA;  20763 MW;  A56CE4EC51D41F8A CRC64;

  Query Match           98.0%;  Score 987;  DB 2;  Length 192;
  Best Local Similarity  98.9%;  Pred. No. 2.6e-80;
  Matches  188;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 61

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 121

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 181

Qy        181 GALVTVGAFF 190
              ||||||||||
Db        182 GALVTVGAFF 191


RESULT 6
Q8CGL4
ID   Q8CGL4       PRELIMINARY;      PRT;   193 AA.
AC   Q8CGL4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Bcl2-like protein 2.
GN   Name=Bcl2l2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL; TISSUE=Skin;
RA   Su H.-Y., Cheng W.T.K., Chen S.C., Lin C.T., Lien Y.Y., Liu H.J.,
RA   Gilmour R.S.;
RT   "Mouse keratinocytes express c98, a novel gene homologous to bcl-2,
RT   that is stimulated by insulin-like growth factor 1 and prevents
RT   dexamethasone-induced apoptosis.";
RL   Biochim. Biophys. Acta 1676:127-137(2004).
DR   EMBL; AY170344; AAO13177.2; -.
DR   HSSP; Q92843; 1O0L.
DR   MGD; MGI:108052; Bcl2l2.
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DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006915; P:apoptosis; IDA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
SQ   SEQUENCE   193 AA;  20958 MW;  60D7F9E4DC56DFAE CRC64;

  Query Match             94.4%;  Score 951;  DB 2;  Length 193;
  Best Local Similarity   94.8%;  Pred. No. 4.4e-77;
  Matches  183;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| |||||||| ||||:||||||||||||||||||||||||||||| :||||||
Db          1 MATPASTPDTRALVAYFVGYQLRQKGYVCGAGPGEGPAADPLHQAMRAAGDELQTRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              || ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 FSHLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKHMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:|||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVAYLETRLAYWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||  |
Db        181 GALVTVGAFFAYK 193


RESULT 7
Q8CFR2
ID   Q8CFR2      PRELIMINARY;      PRT;   178 AA.
AC   Q8CFR2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Bcl2l2 protein.
GN   Name=Bcl2l2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC040369; AAH40369.1; -.
DR   HSSP; Q92843; 1O0L.
DR   MGD; MGI:108052; Bcl2l2.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006915; P:apoptosis; IDA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   178 AA;  19119 MW;  E2C3F3F79528E9D7 CRC64;

  Query Match             75.6%;  Score 761;  DB 2;  Length 178;
  Best Local Similarity   95.3%;  Pred. No. 4.1e-60;
  Matches  143;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTAL 150
              |||:|||||||||||||||||||   : |
Db        121 QVQDWMVAYLETRLADWIHSSGGWVRSSQL 150


RESULT 8
Q9CYW5
ID   Q9CYW5      PRELIMINARY;      PRT;   178 AA.
AC   Q9CYW5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
DE   enriched library, clone:2810435A13 product:Bcl2-like 2, full insert
DE   sequence.
GN   Name=Bcl2l2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
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RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK013244; BAB28740.1; -.
DR   HSSP; Q92843; 1O0L.
DR   MGD; MGI:108052; Bcl2l2.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006915; P:apoptosis; IDA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   178 AA;  19147 MW;  E2D4C3F79528E9D7 CRC64;

  Query Match             75.6%;  Score 761;  DB 2;  Length 178;
  Best Local Similarity   95.3%;  Pred. No. 4.1e-60;
  Matches  143;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTAL 150
              |||:||||||||||||||||||||   : |
Db        121 QVQDWMVAYLETRLADWIHSSGGWVRSSQL 150


RESULT 9
Q6GP82
ID   Q6GP82      PRELIMINARY;      PRT;   188 AA.
AC   Q6GP82;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MGC80617 protein.
GN   Name=MGC80617;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073259; AAH73259.1; -.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
SQ   SEQUENCE   188 AA;  20441 MW;  CB3C1A8C55F16B96 CRC64;

  Query Match             64.7%;  Score 651.5;  DB 2;  Length 188;
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  Best Local Similarity   68.9%;  Pred. No. 2.8e-50;
  Matches  126;  Conservative   20;  Mismatches   34;  Indels    3;  Gaps    1;

Qy         11 RALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHV 70
              |||| ||| ||| |:  |       |||:  || |||||||||| |||: ||::: |:||
Db          9 RALVEDFVRYKLCQRSLV---PEPAGPASCALHSAMRAAGDEFEERFRQAFSEISTQIHV 65

Qy         71 TPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYL 130
              |||:|  || :|:  ||||| ||||:|||||||||||||||||| ||: ::|:||| ||
Db         66 TPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTYL 125

Qy        131 ETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFF 190
              || |  || |:|||  |  ||||||:||||| |||||||::||||||||||||:|||| |
Db        126 ETNLRGWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGALF 185

Qy        191 ASK 193
              |||
Db        186 ASK 188


RESULT 10
AR1_XENLA
ID   AR1_XENLA      STANDARD;      PRT;   228 AA.
AC   Q91827;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   29-MAR-2004 (Rel. 43, Last annotation update)
DE   Apoptosis regulator R1 (XR1) (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Head;
RX   MEDLINE=95331613; PubMed=7607538; DOI=10.1016/0378-1119(95)00159-4;
RA   Cruz-Reyes J., Tata J.R.;
RT   "Cloning, characterization and expression of two Xenopus bcl-2-like
RT   cell-survival genes.";
RL   Gene 158:171-179(1995).
CC   -!- FUNCTION: Could be the homolog of mammalian Bcl-W.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC   -!- DEVELOPMENTAL STAGE: Developmental regulation only occurs in the
CC       brain of mid-metamorphosic to post-metamorphosic tadpoles and
CC       adults, where an increase of several fold has been observed.
CC   -!- SIMILARITY: Belongs to the Bcl-2 family.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X82462; CAA57845.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
KW   Apoptosis; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN      120    139       BH1.
FT   DOMAIN      171    186       BH2.
FT   TRANSMEM    207    227       Potential.

SQ   SEQUENCE   228 AA;  25068 MW;  C499D449A585F8A9 CRC64;

  Query Match             64.2%;  Score 646.5;  DB 1;  Length 228;
  Best Local Similarity   67.9%;  Pred. No. 9.6e-50;
  Matches  125;  Conservative   21;  Mismatches   35;  Indels    3;  Gaps    1;

Qy         10 TRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLH 69
              :|||| | | ||| |:  |       | |:  || |||||||||| |||: ||::: |:|
Db         48 SRALVEDLVRYKLCQRSLV---PEPSGAASCALHSAMRAAGDEFEERFRQAFSEISTQIH 104

Qy         70 VTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAY 129
              ||||:|  || :|:  ||||| ||||:|||||||||||||||||| ||: ::|:||| |
Db        105 VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY 164

Qy        130 LETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAF 189
              ||| | ||| |:|||  |  ||||||:||||| |||||||::||||||||||:||||
Db        165 LETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL 224

Qy        190 FASK 193
              ||||
Db        225 FASK 228


RESULT 11
Q9MYW4
ID   Q9MYW4      PRELIMINARY;      PRT;   233 AA.
AC   Q9MYW4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Bcl-X.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Knott J.C., Robertson L., James E.R.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY005131; AAF88137.1; -.
DR   HSSP; P53563; 1AF3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR004725; Bcl2_reg.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   TIGRFAMs; TIGR00865; bcl-2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   233 AA;  25986 MW;  12F0F30344D53F93 CRC64;

  Query Match             43.7%;  Score 440.5;  DB 2;  Length 233;
  Best Local Similarity   42.0%;  Pred. No. 2.7e-31;
  Matches   94;  Conservative   22;  Mismatches   57;  Indels   51;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGYVC--------------GAG---------------PGEGPAA 39
              | || ||: ||| ||||                | |               | : ||
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTGPEMETPSAINGNPAWHPADSPAV 65

Qy         40 D-----------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
              :                 : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db         66 NGATGHSSSLDAREVIPMTAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125

Qy         82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
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                | :|||: | ||||:|||| || ||| |||:|||| || ::  ||  ||   |  ||  :
Db        126 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMEVLVSRIAAWMATYLNDHLEPWIQEN 185

Qy        142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                |||  |  |||: |  |:|: :|    |      : | | ||:|
Db        186 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT 12
Q8SQ42
ID   Q8SQ42      PRELIMINARY;      PRT;   233 AA.
AC   Q8SQ42;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Bcl-xl protein.
GN   Name=bcl-xl;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Nagafuchi S., Sano J., Kano R., Hasegawa A.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB080951; BAB85856.2; -.
DR   HSSP; Q07817; 1MAZ.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR004725; Bcl2_reg.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   TIGRFAMs; TIGR00865; bcl-2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   233 AA;  26017 MW;  CD17F24FE9D47BC9 CRC64;

  Query Match             43.0%;  Score 433.5;  DB 2;  Length 233;
  Best Local Similarity   41.6%;  Pred. No. 1.1e-30;
  Matches   97;  Conservative   23;  Mismatches   58;  Indels   55;  Gaps    5;

Qy         11 RALVADFVGYKLRQKGY----------------------------------------V 28
              | || ||: ||| ||||                                        |
Db          6 RELVVDFLSYKLSQKGYSWSRFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy         29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
               ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db         66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy         81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
              || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db        125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE 184

Qy        141 SGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
              :|||  |  |||: |  |:|:   |   | |  |||    | :| :|: |: |
Db        185 NGGWDTFVELYGNNAAAESRK---GQERSNRWFLTGMTVAG-VVLLGSLFSRK 233


RESULT 13
BCLX_CHICK
ID   BCLX_CHICK     STANDARD;      PRT;   229 AA.
AC   Q07816; Q98908;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
GN   Name=BCL2L1; Synonyms=BCL-X, BCLX;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RX   MEDLINE=93364977; PubMed=8358789; DOI=10.1016/0092-8674(93)90508-N;
RA   Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA   Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT   "bcl-x, a bcl-2-related gene that functions as a dominant regulator of
RT   apoptotic cell death.";
RL   Cell 74:597-608(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM LONG).
RC   STRAIN=Hubbard White Mountain; TISSUE=Testis;
RX   MEDLINE=97264485; PubMed=9110311;
RX   DOI=10.1002/(SICI)1098-2795(199705)47:1<26::AID-MRD4>3.3.CO;2-V;
RA   Vilagrasa X., Mezquita C., Mezquita J.;
RT   "Differential expression of bcl-2 and bcl-x during chicken
RT   spermatogenesis.";
RL   Mol. Reprod. Dev. 47:26-29(1997).
CC   -!- FUNCTION: Dominant regulator of apoptotic cell death. The long
CC       form displays cell death repressor activity, whereas the short
CC       isoform promotes apoptosis (By similarity).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC       envelope (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Long;
CC         IsoId=Q07816-1; Sequence=Displayed;
CC       Name=Short;
CC         IsoId=Q07816-2; Sequence=VSP_000514;
CC   -!- TISSUE SPECIFICITY: Highest expression in organs with lymphoid
CC       development.
CC   -!- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC       function. Intact BH1 and BH2 domains are required for anti-
CC       apoptotic activity (By similarity).
CC   -!- SIMILARITY: Belongs to the Bcl-2 family.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z23110; CAA80657.1; -.
DR   EMBL; U26645; AAB07677.1; -.
DR   PIR; A47537; A47537.
DR   HSSP; P53563; 1AF3.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR004725; Bcl2_reg.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   TIGRFAMs; TIGR00865; bcl-2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Alternative splicing; Apoptosis; Transmembrane.
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FT   DOMAIN        4     24       BH4.
FT   DOMAIN       82     96       BH3.
FT   DOMAIN      125    144       BH1.
FT   DOMAIN      176    191       BH2.
FT   TRANSMEM    206    223       Potential.
FT   VARSPLIC    185    229       ERFVDLYGNNAAAELRKGQETFNKWLLTGATVAGVLLLGSL
FT                                LSRK -> VRTALP (in isoform Short).
FT                                /FTId=VSP_000514.
SQ   SEQUENCE   229 AA;  25733 MW;  A97D3A4D04C0E9DA CRC64;

  Query Match             42.9%;  Score 432.5;  DB 1;  Length 229;
  Best Local Similarity   41.7%;  Pred. No. 1.4e-30;
  Matches   95;  Conservative   22;  Mismatches   62;  Indels   49;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGY----------------------VCGAGPGEGP---------- 37
              | || ||| ||| |:|:                      |    |   |
Db          6 RELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65

Qy         38 ------------AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                         |  : ||:| |||||| |:|| |||| :|||:|||:| | | || :|
Db         66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE 125

Qy         86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
              ||  | ||||:|||| || ||| |||:|||  |||::  ||  ||   |  ||  :|||
Db        126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWE 185

Qy        146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
              |  |||: |   |  ||:|     : :||||   | |: :|:  : |
Db        186 RFVDLYGNNA---AAELRKGQETFNKWLLTGATVAGVLL-LGSLLSRK 229


RESULT 14
BCLX_PIG
ID   BCLX_PIG       STANDARD;      PRT;   233 AA.
AC   O77737;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
GN   Name=BCL2L1; Synonyms=BCLX, BLC2L;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99171363; PubMed=10072723; DOI=10.1006/jmcc.1998.0855;
RA   Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT   "Quantification of cardioprotective gene expression in porcine short-
RT   term hibernating myocardium.";
RL   J. Mol. Cell. Cardiol. 31:147-158(1999).
CC   -!- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-
CC       apoptotic activity is inhibited by association with SIVA isoform
CC       1.Inhibits activation of caspases (By similarity). Appears to
CC       regulate cell death by blocking the voltage-dependent anion
CC       channnel (VDAC) by binding to it and preventing the release of the
CC       caspase activator, cytochrome c, from the mitochondrial membrane.
CC   -!- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC       similarity). Heterodimerization with BAX does not seem to be
CC       required for anti-apoptotic activity (By similarity). Isoform Bcl-
CC       X(L) binds to Siva isoform 1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC       envelope (By similarity).
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC       The BH1 and BH2 domains are required for both heterodimerization
CC       with other Bcl-2 family members and for repression of cell death.
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis (By
CC       similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC       apoptotic activity (By similarity).
CC   -!- SIMILARITY: Belongs to the Bcl-2 family.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ001203; CAA04597.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR004725; Bcl2_reg.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   TIGRFAMs; TIGR00865; bcl-2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Mitochondrion; Transmembrane.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       Potential.
SQ   SEQUENCE   233 AA;  26061 MW;  18BF6FA0441912B2 CRC64;

  Query Match             42.9%;  Score 431.5;  DB 1;  Length 233;
  Best Local Similarity   41.8%;  Pred. No. 1.7e-30;
  Matches   94;  Conservative   21;  Mismatches   57;  Indels   53;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGY-------------------------------------------V 28
              | || ||: ||| ||||                                           |
Db          6 RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65

Qy         29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db         66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy         81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
              || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db        125 QVLNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE 184

Qy        141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
              :|||  |  |||: |  |:|: :|    |       | | | ||:|
Db        185 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL 229


RESULT 15
Q9N1A2
ID   Q9N1A2      PRELIMINARY;      PRT;   233 AA.
AC   Q9N1A2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Anti-apoptotic regulator Bcl-xL.
GN   Name=bcl-xL;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RA   Lee T.L., Canty J.M.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF216205; AAF33212.1; -.
```

```
DR   HSSP; Q07817; 1R2D.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR004725; Bcl2_reg.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   TIGRFAMs; TIGR00865; bcl-2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   233 AA;  26047 MW;  2FA312818B25E17D CRC64;

  Query Match             42.9%;  Score 431.5;  DB 2;  Length 233;
  Best Local Similarity   41.8%;  Pred. No. 1.7e-30;
  Matches   94;  Conservative   21;  Mismatches   57;  Indels   53;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGY----------------------------------------V 28
              | || ||: ||| ||||                                        |
Db          6 RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65

Qy         29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
               ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db         66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy         81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
              || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db        125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE 184

Qy        141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
              :|||  |  |||: |  |:|: :|    |       | | | ||:|
Db        185 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL 229

Search completed: April 10, 2005, 22:42:53
Job time : 61 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 10, 2005, 20:12:38 ; Search time 65 Seconds
(without alignments)
1148.381 Million cell updates/sec

Title: US-09-925-674B-7
Perfect score: 1007
Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1007	100.0	193	2	AAY05530	Aay05530 Human Bcl
2	1007	100.0	193	7	ADD46742	Add46742 Human Pro
3	1007	100.0	193	8	ADP88349	Adp88349 Human Bcl
4	1002	99.5	193	2	AAW61392	Aaw61392 Human bcl
5	1002	99.5	193	2	AAW97392	Aaw97392 The human
6	1000	99.3	193	2	AAW36047	Aaw36047 Human bcl
7	1000	99.3	193	2	AAY05532	Aay05532 Human Bcl
8	1000	99.3	193	2	AAY05531	Aay05531 Mouse Bcl
9	997	99.0	192	2	AAW97394	Aaw97394 Mammalian
10	996	98.9	193	2	AAW61391	Aaw61391 Rat bcl-y
11	996	98.9	193	2	AAW97391	Aaw97391 The rat b
12	991	98.4	192	2	AAW97393	Aaw97393 Protein s
13	958.5	95.2	192	2	AAY05533	Aay05533 Mouse Bcl
14	954	94.7	183	8	ADP88350	Adp88350 Derivativ
15	867	86.1	168	2	AAW36048	Aaw36048 Mouse bcl
16	821.5	81.6	190	5	AAO18223	Aao18223 Human Bcl
17	766	76.1	365	2	AAW59884	Aaw59884 Amino aci
18	766	76.1	365	5	ABG95556	Abg95556 Human nov
19	766	76.1	365	6	ABO34750	Abo34750 Fragment
20	766	76.1	365	7	ADI23411	Adi23411 Novel hum
21	766	76.1	365	8	ADH74413	Adh74413 Human sec
22	764.5	75.9	185	8	ABM84148	Abm84148 Human dia
23	457.5	45.4	179	8	ADH52635	Adh52635 Chinese h
24	448.5	44.5	199	8	ADH52637	Adh52637 Chinese h
25	441.5	43.8	219	8	ADH52639	Adh52639 Chinese h
26	436.5	43.3	219	8	ADH52641	Adh52641 Chinese h
27	435.5	43.2	342	8	ADQ97763	Adq97763 Mouse can
28	433.5	43.0	411	4	AAU00219	Aau00219 Bcl-Xl-DT
29	431.5	42.9	233	8	ADQ80679	Adq80679 Porcine a
30	431.5	42.9	237	5	ABG78480	Abg78480 Wild type
31	429.5	42.7	233	8	ADH52633	Adh52633 Chinese h
32	428.5	42.6	233	2	AAR68887	Aar68887 Human thy
33	428.5	42.6	233	2	AAW05821	Aaw05821 Bcl-XL pr
34	428.5	42.6	233	2	AAW31530	Aaw31530 Human ant
35	428.5	42.6	233	3	AAY69969	Aay69969 Human Bcl
36	428.5	42.6	233	3	AAY83223	Aay83223 Bcl-x pol
37	428.5	42.6	233	4	AAB50538	Aab50538 Human Bcl
38	428.5	42.6	233	4	AAB73303	Aab73303 Rat wild-
39	428.5	42.6	233	4	AAG64262	Aag64262 Human Bcl
40	428.5	42.6	233	4	AAB47515	Aab47515 Protein e
41	428.5	42.6	233	7	ADE62921	Ade62921 Rat Prote
42	428.5	42.6	233	7	ADE62493	Ade62493 Human Pro
43	428.5	42.6	233	7	ADE62491	Ade62491 Rat Prote
44	428.5	42.6	233	7	ABW02410	Abw02410 Human bcl
45	428.5	42.6	233	8	ADM45995	Adm45995 Human apo

ALIGNMENTS

RESULT 1
AAY05530
ID AAY05530 standard; protein; 193 AA.
XX
AC AAY05530;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human Bcl-w protein essential for spermatogenesis.
XX
KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW animal model.
XX
OS Homo sapiens.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
DR WPI; 1999-243890/20.
DR N-PSDB; AAX25132.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w.
XX
PS Claim 2; Page 33; 52pp; English.
XX
CC The present sequence is human Bcl-w, a pro-survival member of the Bcl-2
CC family which is widely expressed and which is essential for
CC spermatogenesis. The invention relates generally to a method of treatment
CC and to an animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for reducing
CC fertility, by modulating spermatogenesis. An animal model carries a
CC mutation is at least one allele of the human or murine bcl-w gene (see
CC AAX25132-35) or in a gene associated with bcl-w. Such animals have
CC disorganised seminferous tubules and are substantially infertile, but
CC possess no other major abnormalities as determined by histological
CC examination. They can be used to screen for therapeutic molecules
CC including genetic sequences capable of inducing, enhancing or otherwise

```
CC   facilitating spermatogenesis in animals, or which can induce infertility
XX
SQ   Sequence 193 AA;

  Query Match             100.0%;  Score 1007;  DB 2;  Length 193;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-102;
  Matches  193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 2
ADD46742
ID   ADD46742 standard; protein; 193 AA.
XX
AC   ADD46742;
XX
DT   02-DEC-2004  (revised)
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein Q92843, SEQ ID NO 12427.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; Q92843.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Example 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (described in Table 3
CC   of the specification) which is differentially expressed during pain.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 193 AA;

  Query Match             100.0%;  Score 1007;  DB 7;  Length 193;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-102;
  Matches  193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 3
ADP88349
ID   ADP88349 standard; protein; 193 AA.
XX
AC   ADP88349;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human Bcl-w protein.
XX
KW   Bcl-w; human; protein structure; protein co-ordinate data.
XX
OS   Homo sapiens.
XX
PN   WO2004050697-A1.
XX
PD   17-JUN-2004.
XX
PF   03-DEC-2003; 2003WO-AU001624.
XX
PR   03-DEC-2002; 2002AU-00953259.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Hinds MG,  Huang DCS,  Day CL;
XX
DR   WPI; 2004-487529/46.
XX
PT   Solution useful for identifying or selecting agents that are capable of
```

PT inhibiting biological activity of Bcl-w, comprises molecule that has Bcl-
PT w active site defined by specific structure coordinates of Bcl-w amino
PT acid residues.
XX
PS Disclosure; Page 804-805; 810pp; English.
XX
CC The present invention relates to a solution comprising a molecule or
CC molecular complex that comprises at least a fragment of Bcl-w. Also
CC disclosed is the structure of Bcl-w, in the form of protein coordinate
CC data. The solution is useful for identifying, selecting or designing
CC agents that are capable of inhibiting or potentiating one or more
CC biological activity of Bcl-w, and in solving the structures of other
CC proteins with similar structure. It is also useful for characterizing the
CC three-dimensional structure of the Bcl-w molecule, molecular complex or
CC its derivative. The present sequence is the human Bcl-w protein.
XX
SQ Sequence 193 AA;

Query Match 100.0%; Score 1007; DB 8; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.8e-102;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193
```

RESULT 4
AAW61392
ID AAW61392 standard; protein; 193 AA.
XX
AC AAW61392;
XX
DT 02-OCT-1998 (first entry)
XX
DE Human bcl-y protein.
XX
KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
XX
OS Homo sapiens.
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97US-00798897.
XX
PR 23-FEB-1996; 96US-0012201P.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1998-446079/38.
DR N-PSDB; AAV28334.
XX
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
PT recombinant protein for use in treating uncontrolled cell growth e.g.
PT cancers.
XX
PS Example; Column 17/18; 27pp; English.
XX
CC The mammalian bcl-y protein is a member of the bcl-2 family, components
CC in the cell death pathway. The bcl-2 family have both apoptotic activity
CC and the apoptosis blocking activity. bcl-y falls in the apoptosis
CC activity category. The recombinant protein may be used to prevent
CC uncontrolled cell growth, either by its direct administration to
CC recombinant genetic constructs to increase its expression in vivo. Also,
CC antisense constructs can be used in disorders where prevention of cell
CC death is desired
XX
SQ Sequence 193 AA;

Query Match 99.5%; Score 1002; DB 2; Length 193;
Best Local Similarity 99.5%; Pred. No. 6.6e-102;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193
```

RESULT 5
AAW97392
ID AAW97392 standard; protein; 193 AA.
XX
AC AAW97392;
XX
DT 20-MAY-1999 (first entry)
XX
DE The human bcl-y protein.
XX
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
OS Homo sapiens.
XX
PN US5883229-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-00978523.
XX
PR 23-FEB-1996; 96US-0012201P.
PR 11-FEB-1997; 97US-00798897.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1999-214150/18.
DR N-PSDB; AAX15946.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT modulating programmed cell death.
XX
PS Claim 1; Col 17-18; 26pp; English.

XX
CC The present sequence represents human bcl-y protein (Hbcl-y). The
CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-
CC y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC - conditions where cells under go premature cell death as a result of
CC triggers which may or may not be apparent. They may also be used in this
CC way to develop cell lines which remain viable in culture for an extended
CC period. In contrast, if they act as cell death stimulators, Rbcl-y and
CC Hbcl-y may be used to treat conditions associated with prolonged cell
CC life span such as cancer (especially kaposi's sarcoma and lung cancer)
CC and auto/hyperimmune diseases. They may also be used to cause cell death
CC in, and hence control, parasites
XX
SQ Sequence 193 AA;

Query Match 99.5%; Score 1002; DB 2; Length 193;
Best Local Similarity 99.5%; Pred. No. 6.6e-102;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193
```

RESULT 6
AAW36047
ID AAW36047 standard; protein; 193 AA.
XX
AC AAW36047;
XX
DT 22-APR-1998 (first entry)
XX
DE Human bcl-w protein.
XX
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease.
XX
OS Homo sapiens.
XX
PN WO9735971-A1.
XX
PD 02-OCT-1997.
XX
PF 27-MAR-1997; 97WO-AU000199.
XX
PR 27-MAR-1996; 96AU-00008965.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Cory S, Adams JM, Gibson LM, Holmgreen SP;
XX
DR WPI; 1997-489635/45.
DR N-PSDB; AAT96577.
XX
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
PT inhibit cell survival, e.g. for treatment of cancer and degenerative
PT diseases.
XX
PS Claim 6; Page 48; 86pp; English.
XX
CC This sequence represents a novel human protein, bcl-w, encoded by the bcl
CC -2 gene family and extracted from an adult brain library. This gene
CC promotes cell survival, so its modulation is useful in treatment of
CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
CC ischaemia, human immunodeficiency virus infection or in cell transplants.
CC Up-regulation of the gene can also be used to modify cell lines cultured
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
CC and to increase survival of primary explants during genetic modification.
CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
CC antibody production or screening of potential modulators
XX
SQ Sequence 193 AA;

Query Match 99.3%; Score 1000; DB 2; Length 193;
Best Local Similarity 99.0%; Pred. No. 1.1e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193
```

RESULT 7
AAY05532
ID AAY05532 standard; protein; 193 AA.
XX
AC AAY05532;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human Bcl-w protein essential for spermatogenesis.
XX
KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW animal model.
XX
OS Homo sapiens.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
DR WPI; 1999-243890/20.
DR N-PSDB; AAX25134.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w.

```
XX
PS   Disclosure; Page 37; 52pp; English.
XX
CC   The present sequence is described of a derivative of human Bcl-w (see
CC   also AAY05530), a pro-survival member of the Bcl-2 family that is widely
CC   expressed and which is essential for spermatogenesis. The invention
CC   relates generally to a method of treatment and to an animal model for the
CC   identification of molecules and genetic sequences useful for inducing or
CC   reducing fertility of male animals. Methods are provided for the
CC   treatment of infertility, or for reducing fertility, by modulating
CC   spermatogenesis. An animal model carries a mutation is at least one
CC   allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
CC   associated with bcl-w. Such animals have disorganised seminferous tubules
CC   and are substantially infertile, but possess no other major abnormalities
CC   as determined by histological examination. They can be used to screen for
CC   therapeutic molecules including genetic sequences capable of inducing,
CC   enhancing or otherwise facilitating spermatogenesis in animals, or which
CC   can induce infertility
XX
SQ   Sequence 193 AA;

  Query Match             99.3%;  Score 1000;  DB 2;  Length 193;
  Best Local Similarity   99.0%;  Pred. No. 1.1e-101;
  Matches  191;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 8
AAY05531
ID   AAY05531 standard; protein; 193 AA.
XX
AC   AAY05531;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Mouse Bcl-w protein essential for spermatogenesis.
XX
KW   Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW   animal model.
XX
OS   Mus sp.
XX
PN   WO9913710-A1.
XX
PD   25-MAR-1999.
XX
PF   16-SEP-1998;   98WO-AU000764.
XX
PR   16-SEP-1997;   97AU-00009228.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Cory S,  Adams J,  Print C,  Gibson L,  Koentgen F;
XX
DR   WPI; 1999-243890/20.
DR   N-PSDB; AAX25133.
XX
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w.
XX
PS   Claim 2; Page 35; 52pp; English.
XX
CC   The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2
CC   family which is widely expressed and which is essential for
CC   spermatogenesis. The invention relates generally to a method of treatment
CC   and to an animal model for the identification of molecules and genetic
CC   sequences useful for inducing or reducing fertility of male animals.
CC   Methods are provided for the treatment of infertility, or for reducing
CC   fertility, by modulating spermatogenesis. An animal model carries a
CC   mutation is at least one allele of the human or murine bcl-w gene (see
CC   AAX25132-35) or in a gene associated with bcl-w. Such animals have
CC   disorganised seminferous tubules and are substantially infertile, but
CC   possess no other major abnormalities as determined by histological
CC   examination. They can be used to screen for therapeutic molecules
CC   including genetic sequences capable of inducing, enhancing or otherwise
CC   facilitating spermatogenesis in animals, or which can induce infertility
XX
SQ   Sequence 193 AA;

  Query Match             99.3%;  Score 1000;  DB 2;  Length 193;
  Best Local Similarity   99.0%;  Pred. No. 1.1e-101;
  Matches  191;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 9
AAW97394
ID   AAW97394 standard; protein; 192 AA.
XX
AC   AAW97394;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Mammalian bcl-y protein.
XX
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
OS   Mammalia.
XX
PN   US5883229-A.
XX
PD   16-MAR-1999.
XX
PF   25-NOV-1997;   97US-00978523.
XX
PR   23-FEB-1996;   96US-0012201P.
PR   11-FEB-1997;   97US-00798897.
XX
PA   (COCE-) COCENSYS INC.
XX
```

PI Guastella J;
XX
DR WPI; 1999-214150/18.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT modulating programmed cell death.
XX
PS Claim 2; Col 19-22; 26pp; English.
XX
CC The present sequence represents a mammalian bcy-1 protein. The
CC specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
CC thought to be involved in programmed cell death (apoptosis and necrosis).
CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
CC with a disruption of the cell death pathway. If they act as cell death
CC inhibitors, they may be used in therapies to treat subjects suffering
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC degenerative diseases (especially multiple sclerosis), myocardial
CC infarction, vitally induced cell death, aging, spinal cord injuries and
CC amyotrophic lateral sclerosis- conditions where cells under go premature
CC cell death as a result of triggers which may or may not be apparent. They
CC may also be used in this way to develop cell lines which remain viable in
CC culture for an extended period. In contrast, if they act as cell death
CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated
CC with prolonged cell life span such as cancer (especially kaposi's sarcoma
CC and lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites
XX
SQ Sequence 192 AA;

Query Match 99.0%; Score 997; DB 2; Length 192;
Best Local Similarity 99.5%; Pred. No. 2.3e-101;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy    2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
      ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60

Qy   62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120

Qy  122 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

Qy  182 ALVTVGAFFASK 193
      ||||||||||||
Db  181 ALVTVGAFFASK 192
```

RESULT 10
AAW61391
ID AAW61391 standard; protein; 193 AA.
XX
AC AAW61391;
XX
DT 02-OCT-1998 (first entry)
XX
DE Rat bcl-y protein.
XX
KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS Rattus sp.
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97US-00798897.
XX
PR 23-FEB-1996; 96US-0012201P.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1998-446079/38.
DR N-PSDB; AAV28333.
XX
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
PT recombinant protein for use in treating uncontrolled cell growth e.g.
PT cancers.
XX
PS Example; Fig 3A; 27pp; English.
XX
CC The mammalian bcl-y protein is a member of the bcl-2 family, components
CC in the cell death pathway. The bcl-2 family have both apoptotic activity
CC and the apoptosis blocking activity. bcl-y falls in the apoptosis
CC activity category. The recombinant protein may be used to prevent
CC uncontrolled cell growth, either by its direct administration to
CC recombinant genetic constructs to increase its expression in vivo. Also,
CC antisense constructs can be used in disorders where prevention of cell
CC death is desired
XX
SQ Sequence 193 AA;

Query Match 98.9%; Score 996; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 3e-101;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy    1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
      |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy   61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy  121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
      |||:||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy  181 GALVTVGAFFASK 193
      |||||||||||||
Db  181 GALVTVGAFFASK 193
```

RESULT 11
AAW97391
ID AAW97391 standard; protein; 193 AA.
XX
AC AAW97391;
XX
DT 20-MAY-1999 (first entry)
XX
DE The rat bcl-y protein.
XX
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
OS Rattus sp.
XX
PN US5883229-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-00978523.
XX
PR 23-FEB-1996; 96US-0012201P.
PR 11-FEB-1997; 97US-00798897.

XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1999-214150/18.
DR N-PSDB; AAX15945.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT modulating programmed cell death.
XX
PS Disclosure; Col 15-18; 26pp; English.
XX
CC The present sequence represents rat bcl-y protein (Rbcl-y). The
CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC - conditions where cells under go premature cell death as a result of
CC triggers which may or may not be apparent. They may also be used in this
CC way to develop cell lines which remain viable in culture for an extended
CC period. In contrast, if they act as cell death stimulators, Rbcl-y and
CC Hbcl-y may be used to treat conditions associated with prolonged cell
CC life span such as cancer (especially kaposi's sarcoma and lung cancer)
CC and auto/hyperimmune diseases. They may also be used to cause cell death
CC in, and hence control, parasites
XX
SQ Sequence 193 AA;

Query Match 98.9%; Score 996; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 3e-101;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193
```

RESULT 12
AAW97393
ID AAW97393 standard; protein; 192 AA.
XX
AC AAW97393;
XX
DT 20-MAY-1999 (first entry)
XX
DE Protein sequence of the specification.
XX
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
OS Unidentified.
XX
PN US5883229-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-00978523.
XX
PR 23-FEB-1996; 96US-0012201P.
PR 11-FEB-1997; 97US-00798897.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1999-214150/18.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT modulating programmed cell death.
XX
PS Disclosure; Col 19-20; 26pp; English.
XX
CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
CC thought to be involved in programmed cell death (apoptosis and necrosis).
CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
CC with a disruption of the cell death pathway. If they act as cell death
CC inhibitors, they may be used in therapies to treat subjects suffering
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC degenerative diseases (especially multiple sclerosis), myocardial
CC infarction, vitally induced cell death, aging, spinal cord injuries and
CC amyotrophic lateral sclerosis- conditions where cells under go premature
CC cell death as a result of triggers which may or may not be apparent. They
CC may also be used in this way to develop cell lines which remain viable in
CC culture for an extended period. In contrast, if they act as cell death
CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated
CC with prolonged cell life span such as cancer (especially kaposi's sarcoma
CC and lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites
XX
SQ Sequence 192 AA;

Query Match 98.4%; Score 991; DB 2; Length 192;
Best Local Similarity 98.4%; Pred. No. 1.1e-100;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60

Qy         62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120

Qy        122 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
              ||:||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

Qy        182 ALVTVGAFFASK 193
              ||||||||||||
Db        181 ALVTVGAFFASK 192
```

RESULT 13
AAY05533
ID AAY05533 standard; protein; 192 AA.
XX
AC AAY05533;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse Bcl-w protein deritvative.
XX

KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW animal model.
XX
OS Mus sp.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
DR WPI; 1999-243890/20.
DR N-PSDB; AAX25135.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w.
XX
PS Disclosure; Page 39; 52pp; English.
XX
CC The present sequence is described of a derivative of mouse Bcl-w (see
CC also AAY05531), a pro-survival member of the Bcl-2 family that is widely
CC expressed and which is essential for spermatogenesis. The derivative
CC lacks the 24 N-terminal amino acids of Bcl-w. The invention relates
CC generally to a method of treatment and to an animal model for the
CC identification of molecules and genetic sequences useful for inducing or
CC reducing fertility of male animals. Methods are provided for the
CC treatment of infertility, or for reducing fertility, by modulating
CC spermatogenesis. An animal model carries a mutation is at least one
CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
CC associated with bcl-w. Such animals have disorganised seminferous tubules
CC and are substantially infertile, but possess no other major abnormalities
CC as determined by histological examination. They can be used to screen for
CC therapeutic molecules including genetic sequences capable of inducing,
CC enhancing or otherwise facilitating spermatogenesis in animals, or which
CC can induce infertility
XX
SQ Sequence 192 AA;

Query Match 95.2%; Score 958.5; DB 2; Length 192;
Best Local Similarity 94.8%; Pred. No. 4.1e-97;
Matches 183; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

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Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              | |||| |||||||||||||:||||||||||||||||||||||||||||||||||||||
Db          1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:|:|||||||||||||||:|||||||||:|||||||||| | ||:||||||
Db        121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        180 GALVTVGAFFASK 192
```

RESULT 14
ADP88350
ID ADP88350 standard; protein; 183 AA.
XX
AC ADP88350;
XX
DT 09-SEP-2004 (first entry)
XX
DE Derivative of human Bcl-w protein.
XX
KW Bcl-w; human; protein structure; protein co-ordinate data; mutant;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 128
FT /note= "wild-type Ala substituted by Glu"
XX
PN WO2004050697-A1.
XX
PD 17-JUN-2004.
XX
PF 03-DEC-2003; 2003WO-AU001624.
XX
PR 03-DEC-2002; 2002AU-00953259.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Hinds MG, Huang DCS, Day CL;
XX
DR WPI; 2004-487529/46.
XX
PT Solution useful for identifying or selecting agents that are capable of
PT inhibiting biological activity of Bcl-w, comprises molecule that has Bcl-
PT w active site defined by specific structure coordinates of Bcl-w amino
PT acid residues.
XX
PS Claim 16; Page 805-806; 810pp; English.
XX
CC The present invention relates to a solution comprising a molecule or
CC molecular complex that comprises at least a fragment of Bcl-w. Also
CC disclosed is the structure of Bcl-w, in the form of protein coordinate
CC data. The solution is useful for identifying, selecting or designing
CC agents that are capable of inhibiting or potentiating one or more
CC biological activity of Bcl-w, and in solving the structures of other
CC proteins with similar structure. It is also useful for characterizing the
CC three-dimensional structure of the Bcl-w molecule, molecular complex or
CC its derivative. The present sequence is a derivative of the human Bcl-w
CC protein.
XX
SQ Sequence 183 AA;

Query Match 94.7%; Score 954; DB 8; Length 183;
Best Local Similarity 99.5%; Pred. No. 1.2e-96;
Matches 182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVEYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GAL 183
              |||
Db        181 GAL 183
```

RESULT 15
AAW36048
ID AAW36048 standard; protein; 168 AA.
XX
AC AAW36048;
XX

DT 22-APR-1998 (first entry)
XX
DE Mouse bcl-w protein.
XX
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease.
XX
OS Mus sp.
XX
PN WO9735971-A1.
XX
PD 02-OCT-1997.
XX
PF 27-MAR-1997; 97WO-AU000199.
XX
PR 27-MAR-1996; 96AU-00008965.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Cory S, Adams JM, Gibson LM, Holmgreen SP;
XX
DR WPI; 1997-489635/45.
DR N-PSDB; AAT96578.
XX
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
PT inhibit cell survival, e.g. for treatment of cancer and degenerative
PT diseases.
XX
PS Claim 6; Page 50-51; 86pp; English.
XX
CC This sequence represents a novel protein, bcl-w, encoded by the mouse bcl
CC -2 gene family. This gene promotes cell survival, so its modulation is
CC useful in treatment of cancer or auto-immune diseases, degenerative
CC diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular
CC degeneration, hypoxia, ischaemia, human immunodeficiency virus infection
CC or in cell transplants. Up-regulation of the gene can also be used to
CC modify cell lines cultured in vivo, e.g. to develop new lines, to
CC facilitate isolation of hybridomas and to increase survival of primary
CC explants during genetic modification. It can be used to produce
CC recombinant Bcl-w for therapy, diagnosis, antibody production or
CC screening of potential modulators
XX
SQ Sequence 168 AA;

Query Match 86.1%; Score 867; DB 2; Length 168;
Best Local Similarity 95.8%; Pred. No. 4.3e-87;
Matches 161; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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              | |||| |||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db          1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWA 168
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Db        121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA 168
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Search completed: April 10, 2005, 22:40:49
Job time : 68 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 10, 2005, 22:43:04 ; Search time 227.5 Seconds
(without alignments)
281.650 Million cell updates/sec

Title: US-09-925-674B-7
Perfect score: 1007
Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1007	100.0	193	9	US-09-925-674A-7	Sequence 7, Appli
2	1007	100.0	193	16	US-10-450-366-6	Sequence 6, Appli
3	997	99.0	193	9	US-09-925-674A-9	Sequence 9, Appli
4	766	76.1	365	10	US-09-809-391-696	Sequence 696, App
5	766	76.1	365	10	US-09-882-171-696	Sequence 696, App
6	766	76.1	365	15	US-10-164-861-696	Sequence 696, App
7	627.5	62.3	228	16	US-10-659-705-2	Sequence 2, Appli
8	457.5	45.4	179	15	US-10-402-017-6	Sequence 6, Appli
9	448.5	44.5	199	15	US-10-402-017-8	Sequence 8, Appli
10	441.5	43.8	219	15	US-10-402-017-10	Sequence 10, Appl
11	436.5	43.3	219	15	US-10-402-017-12	Sequence 12, Appl
12	433.5	43.0	411	16	US-10-792-517-2	Sequence 2, Appli
13	432.5	42.9	229	16	US-10-659-705-7	Sequence 7, Appli
14	429.5	42.7	233	15	US-10-402-017-4	Sequence 4, Appli
15	428.5	42.6	233	9	US-09-734-846-2	Sequence 2, Appli
16	428.5	42.6	233	9	US-09-952-278-6	Sequence 6, Appli
17	428.5	42.6	233	14	US-10-101-482-14	Sequence 14, Appl
18	428.5	42.6	233	14	US-10-072-830-4	Sequence 4, Appli
19	428.5	42.6	233	14	US-10-169-223-10	Sequence 10, Appl
20	428.5	42.6	233	14	US-10-302-262-2	Sequence 2, Appli
21	428.5	42.6	233	15	US-10-116-275-171	Sequence 171, App
22	428.5	42.6	233	16	US-10-450-366-5	Sequence 5, Appli
23	428.5	42.6	233	16	US-10-659-705-8	Sequence 8, Appli
24	416.5	41.4	239	15	US-10-148-953A-3	Sequence 3, Appli
25	415.5	41.3	152	14	US-10-158-769-2	Sequence 2, Appli
26	414.5	41.2	233	16	US-10-659-705-3	Sequence 3, Appli
27	413	41.0	236	13	US-10-087-192-1953	Sequence 1953, Ap
28	412.5	41.0	239	14	US-10-277-693A-10	Sequence 10, Appl
29	412.5	41.0	239	15	US-10-003-632C-10	Sequence 10, Appl
30	412.5	41.0	239	15	US-10-003-632C-13	Sequence 13, Appl
31	410.5	40.8	239	8	US-08-726-211-5	Sequence 5, Appli
32	410.5	40.8	239	10	US-09-993-420A-8	Sequence 8, Appli
33	410.5	40.8	239	14	US-10-101-482-12	Sequence 12, Appl
34	410.5	40.8	239	14	US-10-072-830-2	Sequence 2, Appli
35	410.5	40.8	239	14	US-10-141-618-12	Sequence 12, Appl
36	410.5	40.8	239	14	US-10-053-645A-21	Sequence 21, Appl
37	410.5	40.8	239	15	US-10-387-961A-5	Sequence 5, Appli
38	410.5	40.8	239	15	US-10-003-632C-1	Sequence 1, Appli
39	410.5	40.8	239	15	US-10-003-632C-3	Sequence 3, Appli
40	410.5	40.8	239	15	US-10-148-953A-1	Sequence 1, Appli
41	410.5	40.8	239	15	US-10-148-953A-2	Sequence 2, Appli
42	410.5	40.8	239	15	US-10-297-321-2	Sequence 2, Appli
43	410.5	40.8	239	16	US-10-450-366-4	Sequence 4, Appli
44	410.5	40.8	239	16	US-10-770-668-16	Sequence 16, Appl
45	410.5	40.8	485	16	US-10-792-517-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-925-674A-7
; Sequence 7, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 193
; TYPE: PRT
; ORGANISM: HUMAN
US-09-925-674A-7

Query Match 100.0%; Score 1007; DB 9; Length 193;
Best Local Similarity 100.0%; Pred. No. 7.9e-97;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
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Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 2
US-10-450-366-6
; Sequence 6, Application US/10450366
; Publication No. US20040115667A1
; GENERAL INFORMATION:
;  APPLICANT: Tschopp, Jorg
;  APPLICANT:  Hoffmann, Kay
;  TITLE OF INVENTION: DNA-Sequences, Which Code For An Apoptosis Signal Transduction Pr
;  FILE REFERENCE: 11436*3
;  CURRENT APPLICATION NUMBER: US/10/450,366
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: PCT/EP01/14597
;  PRIOR FILING DATE: 2001-12-12
;  PRIOR APPLICATION NUMBER: DE 100 61 766.2
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: DE 101 00 280.7
;  PRIOR FILING DATE: 2001-01-04
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human Bcl-W
US-10-450-366-6

  Query Match           100.0%;  Score 1007;  DB 16;  Length 193;
  Best Local Similarity  100.0%;  Pred. No. 7.9e-97;
  Matches  193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 3
US-09-925-674A-9
; Sequence 9, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
;  APPLICANT: AMRAD Operations Pty Ltd
;  TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
;  TITLE OF INVENTION:  FAMILY OF APOPTOSIS-CONTROLLING GENES
;  FILE REFERENCE: 11686a
;  CURRENT APPLICATION NUMBER: US/09/925,674A
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/925,674
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: PN8965
;  PRIOR FILING DATE: 1996-03-27
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-925-674A-9

  Query Match           99.0%;  Score 997;  DB 9;  Length 193;
  Best Local Similarity  98.4%;  Pred. No. 8.7e-96;
  Matches  190;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| |||||||||||||:||||||||||||||||||||||||||||||||||||||||
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Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 4
US-09-809-391-696
; Sequence 696, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P2
;  CURRENT APPLICATION NUMBER: US/09/809,391
;  CURRENT FILING DATE:  2001-03-16
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 761
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 696
;   LENGTH: 365
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-809-391-696

  Query Match           76.1%;  Score 766;  DB 10;  Length 365;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-71;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGW 144
              ||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGW 144


RESULT 5
US-09-882-171-696
; Sequence 696, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P2
;  CURRENT APPLICATION NUMBER: US/09/882,171
;  CURRENT FILING DATE:  2001-06-18
```

; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,612
; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
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; PRIOR FILING DATE: 1997-04-11
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; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,674
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,669
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,312
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,313
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,672
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,315
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/056,886
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,877
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,889
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,893
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,630
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,878
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,662
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,872
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,882
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,637
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,903
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,888
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,879
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,880
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,894
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,911
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,636
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,874
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,910
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,864
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,631
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,892
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/047,595
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,588
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,585
; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,590
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match 76.1%; Score 766; DB 10; Length 365;
Best Local Similarity 100.0%; Pred. No. 2.7e-71;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGW 144
              ||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGW 144
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RESULT 6
US-10-164-861-696
, Sequence 696, Application US/10164861
, Publication No. US20030225248A1
, GENERAL INFORMATION:
, APPLICANT: Rosen et al.
, TITLE OF INVENTION: 186 Human Secreted proteins
, FILE REFERENCE: PZ002P1
, CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 696
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-861-696

Query Match 76.1%; Score 766; DB 15; Length 365;
Best Local Similarity 100.0%; Pred. No. 2.7e-71;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQEWMVAYLETRLADWIHSSGGW 144
              ||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGW 144
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RESULT 7
US-10-659-705-2
; Sequence 2, Application US/10659705
; Publication No. US20040117867A1
; GENERAL INFORMATION:
; APPLICANT: Look, A. Thomas
; APPLICANT: Langenau, David M.
; TITLE OF INVENTION: Transgenic Cancer Models in Fish
; FILE REFERENCE: 112706.123
; CURRENT APPLICATION NUMBER: US/10/659,705
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 60/409,585
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BCL2 proteins
US-10-659-705-2

Query Match 62.3%; Score 627.5; DB 16; Length 228;
Best Local Similarity 66.8%; Pred. No. 4.4e-57;
Matches 123; Conservative 21; Mismatches 37; Indels 3; Gaps 1;

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Qy         10 TRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLH 69
              :|||| | | ||| |:  |       | |:  || |||||||||| | |: ||::: |:|
Db         48 SRALVEDLVRYKLCQRSLV---PEPSGAASCALHSAMRAAGDEFEERPRQAFSEISTQIH 104

Qy         70 VTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAY 129
              ||||:|  || :|:  ||||| ||||:|||||||||||||||||| ||: ::|:||| |
Db        105 VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY 164

Qy        130 LETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAF 189
              ||| |  || |:|||  |  |||||||:||||| |||||||::|||||||||||:||||
Db        165 LETNLDRWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL 224

Qy        190 FASK 193
              ||||
Db        225 FASK 228
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```
RESULT 8
US-10-402-017-6
; Sequence 6, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
;  APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
;  TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
;  TITLE OF INVENTION:  such cells
;  FILE REFERENCE: Case 1/1314
;  CURRENT APPLICATION NUMBER: US/10/402,017
;  CURRENT FILING DATE:  2003-03-28
;  PRIOR APPLICATION NUMBER: US 60/369,307
;  PRIOR APPLICATION NUMBER: April 2, 2002
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 179
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del26-83)
US-10-402-017-6

  Query Match             45.4%;  Score 457.5;  DB 15;  Length 179;
  Best Local Similarity   52.0%;  Pred. No. 1.8e-39;
  Matches   91;  Conservative   21;  Mismatches   56;  Indels    7;  Gaps    2;

Qy         11 RALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHV 70
              | || ||: ||| ||||   |      ||  : ||:| |||||| |:|| |||| :|||:
Db          6 RELVVDFLSYKLSQKGYSWSAA-----AAAAVKQALREAGDEFELRYRRAFSDLTSQLHI 60

Qy         71 TPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYL 130
              |||:| | | || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||
Db         61 TPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYL 120

Qy        131 ETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                |  ||  :|||  |  |||: |  |:|: :|    |       : | | ||:|
Db        121 NDHLEPWIQDNGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 175


RESULT 9
US-10-402-017-8
; Sequence 8, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
;  APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
;  TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
;  TITLE OF INVENTION:  such cells
;  FILE REFERENCE: Case 1/1314
;  CURRENT APPLICATION NUMBER: US/10/402,017
;  CURRENT FILING DATE:  2003-03-28
;  PRIOR APPLICATION NUMBER: US 60/369,307
;  PRIOR APPLICATION NUMBER: April 2, 2002
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 199
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del46-83)
US-10-402-017-8

  Query Match             44.5%;  Score 448.5;  DB 15;  Length 199;
  Best Local Similarity   47.9%;  Pred. No. 1.8e-38;
  Matches   91;  Conservative   21;  Mismatches   61;  Indels   17;  Gaps    2;

Qy         11 RALVADFVGYKLRQKGYVC---------------GAGPGEGPAADPLHQAMRAAGDEFET 55
              | || ||: ||| ||||                |      ||  : ||:| ||||||
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESERAAAAAAVKQALREAGDEFEL 65

Qy         56 RFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEM 115
                |:|| |||| :|||:|||:| | | || :|||: | ||||:|||| || ||| |||:|||
Db         66 RYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEM 125

Qy        116 EPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--GNWASVRTV 173
              : || ::  ||  ||   |  ||  :|||  |  |||: |  |:|: :|    |
Db        126 QVLVSRIASWMATYLNDHLEPWIQDNGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMT 185

Qy        174 LTGAVALGAL 183
              : | | ||:|
Db        186 VAGVVLLGSL 195


RESULT 10
US-10-402-017-10
; Sequence 10, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
;  APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
;  TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
;  TITLE OF INVENTION:  such cells
;  FILE REFERENCE: Case 1/1314
;  CURRENT APPLICATION NUMBER: US/10/402,017
;  CURRENT FILING DATE:  2003-03-28
;  PRIOR APPLICATION NUMBER: US 60/369,307
;  PRIOR APPLICATION NUMBER: April 2, 2002
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 219
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del66-83)
US-10-402-017-10

  Query Match             43.8%;  Score 441.5;  DB 15;  Length 219;
  Best Local Similarity   43.3%;  Pred. No. 1.1e-37;
  Matches   91;  Conservative   21;  Mismatches   61;  Indels   37;  Gaps    2;

Qy         11 RALVADFVGYKLRQKGYV----------------------------------CGAGPGE 35
              | || ||: ||| ||||                                    |
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESERETPSAINGNPSWHLADSPAV 65

Qy         36 GPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGR 95
                ||  : ||:| |||||| |:|| |||| :|||:|||:| | | || :|||: | ||||
Db         66 AAAAAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGR 125

Qy         96 LVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGA 155
              :|||| || ||| |||:|||: || ::  ||  ||   |  ||  :|||  |  |||: |
Db        126 IVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQDNGGWDTFVELYGNNA 185

Qy        156 LEEARRLRE--GNWASVRTVLTGAVALGAL 183
                |:|: :|    |       : | | ||:|
Db        186 AAESRKGQERFNRWFLTGMTVAGVVLLGSL 215


RESULT 11
US-10-402-017-12
; Sequence 12, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
;  APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
;  TITLE OF INVENTION: Host cells having improved survival properties and methods to gene
;  TITLE OF INVENTION:  such cells
;  FILE REFERENCE: Case 1/1314
;  CURRENT APPLICATION NUMBER: US/10/402,017
;  CURRENT FILING DATE:  2003-03-28
;  PRIOR APPLICATION NUMBER: US 60/369,307
;  PRIOR APPLICATION NUMBER: April 2, 2002
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 219
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;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del26-83)
US-10-402-017-12

  Query Match           43.3%;  Score 436.5;  DB 15;  Length 219;
  Best Local Similarity  44.1%;  Pred. No. 3.7e-37;
  Matches   93;  Conservative   22;  Mismatches   57;  Indels   39;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGY----------------------------VCGAGPGEGPAAD-- 40
              | || ||: ||| ||||                              | ||  |   : |
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESERAAAAAVNGA-TGHSSSLDAR 64

Qy         41 ------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWG 94
                  : ||:| |||||| |:|| |||| :|||:|||:| | | || :|||: | |||
Db         65 EVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWG 124

Qy         95 RLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDG 154
              |:|||| || ||| |||:|||: || ::  ||  ||    |  ||  :|||  |  |||:
Db        125 RIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQDNGGWDTFVELYGNN 184

Qy        155 ALEEARRLRE--GNWASVRTVLTGAVALGAL 183
              |  |:|: :|    |       : | | ||:|
Db        185 AAAESRKGQERFNRWFLTGMTVAGVVLLGSL 215


RESULT 12
US-10-792-517-2
; Sequence 2, Application US/10792517
; Publication No. US20040152179A1
; GENERAL INFORMATION:
;  APPLICANT: Youle et al.
;  TITLE OF INVENTION: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL
;  TITLE OF INVENTION:  FUSION PROTEIN INHIBITS APOPTOSIS
;  FILE REFERENCE: 4239-55417
;  CURRENT APPLICATION NUMBER: US/10/792,517
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/639,245
;  PRIOR FILING DATE: 2000-08-15
;  PRIOR APPLICATION NUMBER: 60/149,220
;  PRIOR FILING DATE: 1999-08-16
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 411
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: genetic fusion
US-10-792-517-2

  Query Match           43.0%;  Score 433.5;  DB 16;  Length 411;
  Best Local Similarity  39.9%;  Pred. No. 1.7e-36;
  Matches   93;  Conservative   26;  Mismatches   63;  Indels   51;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGY----------------------------VCGAGP----GEGPAA 39
              | || ||: ||| ||||                              |     : ||
Db         26 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 85

Qy         40 D------------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
              :                  : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db         86 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 145

Qy         82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
              | :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||    |  ||  :
Db        146 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQEN 205

Qy        142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGALVTVGAFFAS 192
              |||  |  |||: |  |:|: :|    |       : | | ||:| :  |: |:
Db        206 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRKAYSAA 258


RESULT 13
US-10-659-705-7
; Sequence 7, Application US/10659705
; Publication No. US20040117867A1
; GENERAL INFORMATION:
;  APPLICANT: Look, A. Thomas
;  APPLICANT:  Langenau, David M.
;  TITLE OF INVENTION: Transgenic Cancer Models in Fish
;  FILE REFERENCE: 112706.123
;  CURRENT APPLICATION NUMBER: US/10/659,705
;  CURRENT FILING DATE:  2003-09-11
;  PRIOR APPLICATION NUMBER: US 60/409,585
;  PRIOR FILING DATE: 2002-09-11
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 229
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: BCL2 proteins
US-10-659-705-7

  Query Match           42.9%;  Score 432.5;  DB 16;  Length 229;
  Best Local Similarity  41.7%;  Pred. No. 1e-36;
  Matches   95;  Conservative   22;  Mismatches   62;  Indels   49;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGY----------------------VCGAGPGEGP---------- 37
              | || ||| ||| |:|:                      |    |   |
Db          6 RELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65

Qy         38 ------------AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                         |  : ||:| |||||| |:|| |||| :|||:|||:| | | || :|
Db         66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE 125

Qy         86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
              ||  | ||||:|||| || ||| |||:|||  |||::  ||  ||   |  ||  :|||
Db        126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWE 185

Qy        146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
              |  |||: |   |  ||:|     : :||||   | |: :|:  : |
Db        186 RFVDLYGNNA---AAELRKGQETFNKWLLTGATVAGVLL-LGSLLSRK 229


RESULT 14
US-10-402-017-4
; Sequence 4, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
;  APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
;  TITLE OF INVENTION: Host cells having improved survival properties and methods to gene
;  TITLE OF INVENTION:  such cells
;  FILE REFERENCE: Case 1/1314
;  CURRENT APPLICATION NUMBER: US/10/402,017
;  CURRENT FILING DATE:  2003-03-28
;  PRIOR APPLICATION NUMBER: US 60/369,307
;  PRIOR APPLICATION NUMBER: April 2, 2002
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Cricetulus griseus
US-10-402-017-4

  Query Match           42.7%;  Score 429.5;  DB 15;  Length 233;
  Best Local Similarity  41.3%;  Pred. No. 2.2e-36;
  Matches   93;  Conservative   22;  Mismatches   57;  Indels   53;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGY--------------------------------------------V 28
              | || ||: ||| ||||                                            |
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESERETPSAINGNPSWHLADSPAV 65
```

```
Qy          29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
               ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db          66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy          81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
               || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db         125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQD 184

Qy         141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
               :|||  |  |||: |  |:|: :|    |      : | | ||:|
Db         185 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT 15
US-09-734-846-2
; Sequence 2, Application US/09734846
; Patent No. US20010007025A1
; GENERAL INFORMATION:
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Dean, Nicholas M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Nickoloff, Brian J.
;  APPLICANT:  Zhang, QingQing
;  TITLE OF INVENTION:  Antisense Modulation of bcl-x Expression
;  FILE REFERENCE:  ISPH-0528
;  CURRENT APPLICATION NUMBER: US/09/734,846
;  CURRENT FILING DATE:  2000-12-12
;  PRIOR APPLICATION NUMBER:      09/277,020
;  PRIOR FILING DATE:      1998-03-26
;  PRIOR APPLICATION NUMBER:      09/167,921
;  PRIOR FILING DATE:      1998-10-07
;  PRIOR APPLICATION NUMBER:  09/323,743
;  PRIOR FILING DATE:  1999-06-02
;  NUMBER OF SEQ ID NOS:  74
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-734-846-2

  Query Match           42.6%;  Score 428.5;  DB 9;  Length 233;
  Best Local Similarity   40.6%;  Pred. No. 2.8e-36;
  Matches   91;  Conservative   23;  Mismatches   59;  Indels   51;  Gaps    4;

Qy          11 RALVADFVGYKLRQKGY-------------------------VCGAGP----GEGPAA 39
               | || ||: ||| ||||                         |     : ||
Db           6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy          40 D------------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
               :                  : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db          66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125

Qy          82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
               | :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :
Db         126 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQEN 185

Qy         142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
               |||  |  |||: |  |:|: :|    |      : | | ||:|
Db         186 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


Search completed: April 10, 2005, 22:59:27
Job time : 228.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 10, 2005, 22:09:08 ; Search time 17 Seconds
(without alignments)
1092.343 Million cell updates/sec

Title: US-09-925-674B-7
Perfect score: 1007
Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	428.5	42.6	233	2	B47537	apoptosis regulato
2	428.5	42.6	233	2	I49056	bcl-x long - mouse
3	424.5	42.2	233	2	S51761	BCL-X protein - ra
4	423.5	42.1	233	2	A37332	transforming prote
5	414	41.1	232	2	S24390	transforming prote
6	412.5	41.0	239	1	TVHUA1	transforming prote
7	412	40.9	236	2	I67432	BCL-2 - rat (fragm
8	407	40.4	236	2	I53744	gene bcl-2 protein
9	406	40.3	236	1	TVMSA1	transforming prote
10	404.5	40.2	233	2	I67431	BCL-X-Long - rat
11	403	40.0	236	2	JC7383	B-cell lymphoma 2
12	378	37.5	190	2	A47537	apoptosis regulato
13	377.5	37.5	214	2	I49057	bcl-x transmembran
14	375.5	37.3	227	2	JE0203	apoptosis regulato
15	356	35.4	216	2	B37332	transforming prote
16	349.5	34.7	199	1	TVMSB1	transforming prote
17	346	34.4	205	1	TVHUB1	transforming prote
18	277.5	27.6	154	2	I58194	gene bcl-2 protein
19	182	18.1	170	2	I49055	bcl-x short - mous
20	176	17.5	211	2	S58873	Bak protein - huma
21	174	17.3	176	2	I67435	gene bcl-xshort pr
22	173	17.2	211	2	S58875	cdn-2 protein - hu
23	157.5	15.6	192	2	D47538	bcl-2-associated p
24	153	15.2	192	2	A47538	bcl-2-associated p
25	150	14.9	261	2	H88578	protein ced-9 [imp
26	150	14.9	280	2	A53189	apoptosis suppress
27	149.5	14.8	133	2	I53295	bcl-2-associated p
28	146.5	14.5	179	2	JC7255	Bax-delta protein
29	146.5	14.5	218	2	B47538	bcl-2-associated p
30	143	14.2	177	2	S54778	NR-13 protein - qu
31	141	14.0	255	2	JC7567	Mcl-1a protein - z
32	137.5	13.7	143	2	I38921	bcl-2-associated p
33	118	11.7	175	2	I39055	Bcl-2 related - hu
34	112	11.1	350	2	A47476	BCL2 homolog MCL1
35	105	10.4	172	2	I49449	hemopoietic-specif
36	91.5	9.1	301	2	T36534	probable lipase/es
37	89	8.8	185	2	B83217	hypothetical prote
38	87	8.6	3433	1	GNWVKV	genome polyprotein
39	85	8.4	270	2	AI2598	dihydrodipicolinat
40	85	8.4	279	2	B97381	dihydrodipicolinat
41	84.5	8.4	358	1	AJLCQB	glutamate-ammonia
42	83	8.2	417	2	T39939	DNA binding protei
43	82.5	8.2	1440	1	GNWVJF	genome polyprotein
44	82.5	8.2	3432	1	GNWVJE	genome polyprotein
45	81.5	8.1	354	2	S52040	Gln 1.1 protein -

ALIGNMENTS

RESULT 1
B47537
apoptosis regulator bcl-xL - human
N;Alternate names: bcl-2-related protein
N;Contains: apoptosis regulator bcl-xS
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: B47537; C47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A;Reference number: A47537; MUID:93364977; PMID:8358789
A;Accession: B47537
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 <BOI>
A;Cross-references: UNIPROT:Q07817; GB:L20121; NID:g510900; PIDN:CAA80661.1; PID:g510901
A;Accession: C47537
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-69,'G',71-125,189-233 <BO2>
A;Cross-references: GB:L20122; NID:g623236; PIDN:CAA80662.1; PID:g623237
C;Genetics:
A;Gene: GDB:BCL2L
A;Cross-references: GDB:228079
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; apoptosis
F;1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>
F;1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <MA2>

Query Match 42.6%; Score 428.5; DB 2; Length 233;
Best Local Similarity 40.6%; Pred. No. 1.4e-32;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

```
Qy          11 RALVADFVGYKLRQKGY----------------------------VCGAGP----GEGPAA 39
               | || ||: ||| ||||                            |     : ||
Db           6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy          40 D------------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
               :                  : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db          66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125

Qy          82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
               | :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :
Db         126 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQEN 185

Qy         142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
               |||  |  |||: |  |:|: :|    |       : | | ||:|
Db         186 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
```

RESULT 2

I49056
bcl-x long - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49056; S52866
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A;Reference number: I49055; MUID:95052604; PMID:7963517
A;Accession: I49056
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 <RES>
A;Cross-references: UNIPROT:Q64373; EMBL:U10101; NID:g506647; PIDN:AAA82173.1; PID:g5066
R;Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
submitted to the EMBL Data Library, November 1994
A;Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line throu
A;Reference number: S52866
A;Accession: S52866
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-233 <KAM>
A;Cross-references: EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PID:g695623
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.6%; Score 428.5; DB 2; Length 233;
Best Local Similarity 41.3%; Pred. No. 1.4e-32;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

```
Qy          11 RALVADFVGYKLRQKGY----------------------------------------V 28
               | || ||: ||| ||||                                        |
Db           6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy          29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
               ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db          66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy          81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
               || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db         125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy         141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
               :|||  |  |||: |  |:|: :|    |       : | | ||:|
Db         185 NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
```

RESULT 3
S51761
BCL-X protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51761; S51762
R;Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994
A;Reference number: S51761
A;Accession: S51761
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <MIC>
A;Cross-references: UNIPROT:P53563; EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g6071
A;Experimental source: embryonic; brain
A;Accession: S51762
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125,189-233 <MI2>
A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PID:g607178
A;Experimental source: embryonic; brain
A;Note: smaller form due to splicing
C;Genetics:
A;Introns: 125/3
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.2%; Score 424.5; DB 2; Length 233;
Best Local Similarity 41.3%; Pred. No. 3.4e-32;
Matches 92; Conservative 22; Mismatches 56; Indels 53; Gaps 4;

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Qy          13 LVADFVGYKLRQKGY----------------------------------------VCG 30
               || ||: ||| ||||                                        | |
Db           8 LVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAVNG 67

Qy          31 AGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQV 82
               |  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | | ||
Db          68 A-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQV 126

Qy          83 SDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSG 142
               :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :|
Db         127 VNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENG 186

Qy         143 GWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
               ||  |  |||: |  |:|: :|    |       : | | ||:|
Db         187 GWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
```

RESULT 4
A37332
transforming protein (bcl-2-alpha) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A37332; S35453
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: A37332
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-233 <EGU>
A;Cross-references: UNIPROT:Q00709; EMBL:D11381
C;Genetics:
A;Introns: 189/3
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 42.1%; Score 423.5; DB 2; Length 233;
Best Local Similarity 38.0%; Pred. No. 4.2e-32;
Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;

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Qy           9 DTRALVADFVGYKLRQKGYVCGAG-------PGEGPAADP------------------- 41
               | | :|  :: ||| |:||   ||       |   ||| |
Db          10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69

Qy          42 -----------------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSD 84
                              :| |:| |||||  |:: |  |: :: |||:|| :|  ||  | :
Db          70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129

Qy          85 ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGW 144
               |||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   | :||  :|||
Db         130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW 189

Qy         145 AEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                  |  |||:       | | : :| |::|:|:  | :|| :|:||:   |
Db         190 DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 233
```

RESULT 5
S24390
transforming protein (Bcl-2) homolog - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S24390
R;Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
Biochim. Biophys. Acta 1132, 109-113, 1992
A;Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue c
A;Reference number: S24390; MUID:92379084; PMID:1511008
A;Accession: S24390
A;Status: preliminary

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A;Molecule type: mRNA
A;Residues: 1-232 <CAZ>
A;Cross-references: UNIPROT:Q00709; EMBL:Z11961; NID:g62969; PIDN:CAA78018.1; PID:g62970
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: mitochondrion; transmembrane protein

  Query Match             41.1%;  Score 414;  DB 2;  Length 232;
  Best Local Similarity   37.7%;  Pred. No. 3.3e-31;
  Matches   86;  Conservative   32;  Mismatches   62;  Indels   48;  Gaps    4;

Qy          9 DTRALVADFVGYKLRQKGYVCGAG-------PGEGPAADP------------------- 41
              | | :|  :: ||| |:||   ||       |   ||| |
Db         10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPSPPARL 69

Qy         42 ----------------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                            :| |:| ||||| |::| |: :: |||:|| :|  ||  | :|
Db         70 LLVRCPRLRGCAAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTATGRFVAVVEE 129

Qy         86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
              ||: | || |:|||| ||  :| ||||:|| |||  :  ||  ||   | :||  :|||
Db        130 LFRDGVNWVRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGWD 189

Qy        146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
              |  |||:      | | : :| |::|:|:  | :|| :|:||:   |
Db        190 AFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 232


RESULT 6
TVHUA1
transforming protein bcl-2, splice form alpha - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: C37332; A29409; S02452; A24428; A27622; B27622
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: C37332
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-239 <EGU>
A;Cross-references: UNIPROT:P10415
A;Note: this report is a correction
R;Tsujimoto, Y.; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A;Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene
A;Reference number: A29409; MUID:86259760; PMID:3523487
A;Accession: A29409
A;Molecule type: mRNA
A;Residues: 1-95,'A',97-109,'G',111-236,'S',238-239 <TSU>
A;Cross-references: GB:M13994; NID:g179366; PIDN:AAA51813.1; PID:g179367
A;Note: this sequence has been corrected in reference A37332
R;Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeye
EMBO J. 7, 123-131, 1988
A;Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2
A;Reference number: S02452; MUID:88196071; PMID:2834197
A;Accession: S02452
A;Molecule type: mRNA
A;Residues: 1-239 <SET>
R;Cleary, M.L.; Smith, S.D.; Sklar, J.
Cell 47, 19-28, 1986
A;Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglo
A;Reference number: A24428; MUID:87002488; PMID:2875799
A;Accession: A24428
A;Molecule type: mRNA
A;Residues: 1-58,'T',60-116,'R',118-239 <CLE>
A;Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
R;Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhshi, A.
Oncogene Res. 2, 263-275, 1988
A;Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:
A;Reference number: A27622; MUID:88217344; PMID:3285301
A;Accession: A27622
A;Molecule type: mRNA
A;Residues: 1-58,'T',60-239 <HUA>
A;Accession: B27622
A;Molecule type: DNA
A;Residues: 1-6,'S',8-58,'T',60-128,'C',130-239 <HUA2>
A;Note: the sequence was determined from the germline gene
C;Comment: Constitutive expression of BCL2 following t(14:18) chromosomal translocation
C;Genetics:
A;Gene; GDB:BCL2
A;Cross-references: GDB:119031; OMIM:151430
A;Map position: 18q21.3-18q21.3
C;Function:
A;Description: blocks apoptosis in hematopoietic cells
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

  Query Match             41.0%;  Score 412.5;  DB 1;  Length 239;
  Best Local Similarity   37.0%;  Pred. No. 4.7e-31;
  Matches   87;  Conservative   34;  Mismatches   59;  Indels   55;  Gaps    5;

Qy          9 DTRALVADFVGYKLRQKGYVCGAG-------------------PGE-------------- 35
              | | :|  :: ||| |:||   ||                   ||
Db         10 DNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAPGIFSSQPGHTPHPAASRDPVART 69

Qy         36 -------------GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR 78
                          |||  |    :|  :| |||:|  |:|| |:::::|||:|| :|: |
Db         70 SPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR 129

Qy         79 FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWI 138
              |  | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||
Db        130 FATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWI 189

Qy        139 HSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
               :|||  |  |||       | | : :| |::|:|:  |: :|| :|:||:   |
Db        190 QDNGGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239


RESULT 7
I67432
BCL-2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I67432
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equine
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A;Reference number: I53295; MUID:95129487; PMID:7828536
A;Accession: I67432
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-236 <RES>
A;Cross-references: UNIPROT:P49950; EMBL:U34964; NID:g1004378; PIDN:AAA77687.1; PID:g1004
C;Superfamily: bcl apoptosis regulator, inhibitory type

  Query Match             40.9%;  Score 412;  DB 2;  Length 236;
  Best Local Similarity   36.2%;  Pred. No. 5.1e-31;
  Matches   84;  Conservative   34;  Mismatches   62;  Indels   52;  Gaps    3;

Qy          9 DTRALVADFVGYKLRQKGY------------------------------------------ 27
              | | :|  :: ||| |:||
Db         10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRRAPTPGIFSFQPESNRTPAVHRDTAART 69

Qy         28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                   |  |||    |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db         70 SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy         82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
              | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db        130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMYPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy        142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
               |||  |  |||       | | : :| |::|:|:  |: :|| :|:||:   |
Db        190 GGWDAFVELYG----PSMRPLFDFSWQSLKTLLSLAL-VGACITLGAYLGHK 236
```

RESULT 8
I53744
gene bcl-2 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I53744
R;Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
Gene 140, 291-292, 1994
A;Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.
A;Reference number: I53744; MUID:94193015; PMID:8144041
A;Accession: I53744
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-236 <RES>
A;Cross-references: UNIPROT:P49950; GB:L14680; NID:g408946; PIDN:AAA53662.1; PID:g408947
C;Genetics:
A;Gene: bcl-2
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.4%; Score 407; DB 2; Length 236;
Best Local Similarity 35.8%; Pred. No. 1.5e-30;
Matches 83; Conservative 34; Mismatches 63; Indels 52; Gaps 3;

```
Qy          9 DTRALVADFVGYKLRQKGY----------------------------------------- 27
              | | :|  :: ||| |:||
Db         10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART 69

Qy         28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                    |  |||   |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db         70 SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy         82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
              | :|||: | ||||:|||| ||  :|  |||:|| |||  :  ||  ||   |  ||  :
Db        130 VVEELFRDGVNWGRIVAFFEFGGVMCVGSVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy        142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
              |||  |  |||          | | : :| |::|:|:  |: :|| :|:||:   |
Db        190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
```

RESULT 9
TVMSA1
transforming protein bcl-2-alpha - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 28-Jul-2003
C;Accession: A25960; E37332
R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
A;Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homol
A;Reference number: A90893; MUID:87187643; PMID:3032455
A;Accession: A25960
A;Molecule type: DNA
A;Residues: 1-236 <NEG>
A;Cross-references: GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1; PID:g387109
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: E37332
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-33,'E',34-220,'AL',223-236 <EGU>
C;Genetics:
A;Gene: BCL2
A;Introns: 192/3
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane pro

Query Match 40.3%; Score 406; DB 1; Length 236;
Best Local Similarity 37.1%; Pred. No. 1.9e-30;
Matches 86; Conservative 33; Mismatches 61; Indels 52; Gaps 5;

```
Qy          9 DTRALVADFVGYKLRQKGYVCGAG-----------PG---------------------- 34
              | | :|  :: ||| |:||   ||             ||
Db         10 DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHREMAART 69

Qy         35 ---------EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                      |||  |     :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db         70 SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy         82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
              | :|||: | ||||:|||| ||  :|  |||:|| |||  :  ||  ||   |  ||  :
Db        130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy        142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
              |||  |  |||          | | : :| |::|:|:    :|| :|:||:   |
Db        190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLS-LPWVGACITLGAYLGHK 236
```

RESULT 10
I67431
BCL-X-Long - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I67431
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equine onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A;Reference number: I53295; MUID:95129487; PMID:7828536
A;Accession: I67431
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 <RES>
A;Cross-references: UNIPROT:P53563; EMBL:U34963; NID:g1004376; PIDN:AAA77686.1; PID:g1004
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.2%; Score 404.5; DB 2; Length 233;
Best Local Similarity 39.6%; Pred. No. 2.5e-30;
Matches 89; Conservative 22; Mismatches 61; Indels 53; Gaps 4;

```
Qy         11 RALVADFVGYKLRQKGY----------------------------------------V 28
              | ||  ||: ||| ||||                                        |
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV 65

Qy         29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
              ||  |   : |          : ||:| |||||| |:|| |||| :|||:|||:  | |
Db         66 NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFE 124

Qy         81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
              || :|||: | ||||:||   || ||| |||:|||: || ::  ||  ||   |  ||
Db        125 QVVNELFRDGVNWGRIVASSSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy        141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
              :|||  |  |||:    |:|: :|    |       : | | ||:|
Db        185 NGGWDTFVDLYGNNTAPESRKGQERFNRWFLTGMTVAGVVLLGSL 229
```

RESULT 11
JC7383
B-cell lymphoma 2 protein - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7383
R;Tomicic, M.T.; Christmann, M.; Kaina, B.
Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A;Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A;Reference number: JC7383
A;Contents: Ovary
A;Accession: JC7383
A;Molecule type: mRNA
A;Residues: 1-236 <TOM>
A;Cross-references: UNIPROT:Q9JJV8; GB:AJ271720
C;Comment: This protein has anti-apoptotic function, and supports cell survival.

```
C;Genetics:
A;Gene: bcl-2
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: B-cell lymphoma; ovary

  Query Match             40.0%;  Score 403;  DB 2;  Length 236;
  Best Local Similarity   35.3%;  Pred. No. 3.5e-30;
  Matches   82;  Conservative   34;  Mismatches   64;  Indels   52;  Gaps    3;

Qy          9 DTRALVADFVGYKLRQKGY---------------------------------------- 27
              | | :|  :: ||| |:||
Db         10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART 69

Qy         28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                   |   ||    |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db         70 SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy         82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
              | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||    |  ||  :
Db        130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy        142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
              |||  |  |||       | | : :| |::|:|: |: :|| :|:|  :   |
Db        190 GGWDAFVELYG----PSVRPLFDFSWLSLKTLLSLAL-VGACITLGTYLGHK 236


RESULT 12
A47537
apoptosis regulator bcl-x - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A;Reference number: A47537; MUID:93364977; PMID:8358789
A;Accession: A47537
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-190 <BOI>
A;Cross-references: UNIPROT:Q07816; GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1;
C;Superfamily: bcl apoptosis regulator, inhibitory type

  Query Match             37.5%;  Score 378;  DB 2;  Length 190;
  Best Local Similarity   43.8%;  Pred. No. 5.9e-28;
  Matches   81;  Conservative   14;  Mismatches   44;  Indels   46;  Gaps    3;

Qy         11 RALVADFVGYKLRQKGY----------------------VCGAGPGEGP---------- 37
              | || ||| ||| |:|:                      |   |   |
Db          6 RELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65

Qy         38 ------------AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                         |  : ||:| |||||| |:|| |||| :|||:|||:| | | || :|
Db         66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE 125

Qy         86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
              ||  | ||||:|||| || ||| |||:|||  |||::  ||  ||   |  ||  :|||
Db        126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWV 185

Qy        146 EFTAL 150
                |||
Db        186 R-TAL 189


RESULT 13
I49057
bcl-x transmembrane deleted - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49057
R;Pang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A;Reference number: I49055; MUID:95052604; PMID:7963517
A;Accession: I49057
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-214 <RES>
A;Cross-references: UNIPROT:Q64373; EMBL:U10102; NID:g506649; PIDN:AAA82174.1; PID:g50665
C;Genetics:
A;Gene: bcl-x-long
C;Superfamily: bcl apoptosis regulator, inhibitory type

  Query Match             37.5%;  Score 377.5;  DB 2;  Length 214;
  Best Local Similarity   42.8%;  Pred. No. 7.6e-28;
  Matches   80;  Conservative   16;  Mismatches   40;  Indels   51;  Gaps    3;

Qy         11 RALVADFVGYKLRQKGY----------------------------------------V 28
              | || ||: ||| ||||                                        |
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy         29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
              ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db         66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy         81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
              || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db        125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy        141 SGGWAEF 147
              :|||  |
Db        185 NGGWDTF 191


RESULT 14
JE0203
apoptosis regulator bcl-x isoform - human
N;Alternate names: h-bcl-xbeta
C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE0203
R;Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.
Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A;Title: Identification of a human cDNA encoding a novel bcl-x isoform.
A;Reference number: JE0203; MUID:98340865; PMID:9675101
A;Accession: JE0203
A;Molecule type: mRNA
A;Residues: 1-227 <BAN>
A;Cross-references: UNIPROT:Q07817; GB:U72398; NID:g1622940; PIDN:AAB17354.1; PID:g16229
C;Genetics:
A;Gene: bcl-x
A;Map position: 20
C;Superfamily: bcl apoptosis regulator, inhibitory type

  Query Match             37.3%;  Score 375.5;  DB 2;  Length 227;
  Best Local Similarity   40.8%;  Pred. No. 1.3e-27;
  Matches   82;  Conservative   18;  Mismatches   50;  Indels   51;  Gaps    3;

Qy         11 RALVADFVGYKLRQKGY----------------------------------------V 28
              | || ||: ||| ||||                                        |
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy         29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
              ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db         66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy         81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
              || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db        125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE 184

Qy        141 SGGWAEFTALYGDGALEEARR 161
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Db        185 NGGWVRTKPLVCPFSLASGQR 205


RESULT 15
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B37332
transforming protein (bcl-2-beta) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003
C;Accession: B37332; S35452
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: B37332
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-216 <EGU>
A;Cross-references: EMBL:D11381; EMBL:D11382
C;Superfamily: bcl apoptosis regulator, inhibitory type

  Query Match             35.4%;  Score 356;  DB 2;  Length 216;
  Best Local Similarity   38.4%;  Pred. No. 7.8e-26;
  Matches   71;  Conservative   21;  Mismatches   49;  Indels   44;  Gaps    2;

Qy          9 DTRALVADFVGYKLRQKGYVCGAG-------PGEGPAADP------------------- 41
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                               :| |:| |||||  |::| |: :: |||:|| :|  ||  | :
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Qy         85 ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGW 144
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Db        130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW 189

Qy        145 AEFTA 149
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Db        190 VRACA 194

Search completed: April 10, 2005, 22:44:41
Job time : 19 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 14:45:43 ; Search time 3057.74 Seconds
(without alignments)
9206.966 Million cell updates/sec

Title: US-09-925-674B-8
Perfect score: 581
Sequence: 1 atgccgaccccagcctcaac.....gccttttttgctagcaagtg 581

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	581	100.0	581	6	AX022531	AX022531 Sequence
2	581	100.0	581	6	AX030819	AX030819 Sequence
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4	560.2	96.4	3476	10	AF030769	AF030769 Mus muscu
5	549.2	94.5	3442	10	AK172925	AK172925 Mus muscu
6	544.2	93.7	582	10	AF096291	AF096291 Rattus no
7	544.2	93.7	1110	10	AY185100	AY185100 Rattus no
8	544.2	93.7	3487	10	AY185098	AY185098 Rattus no
9	544.2	93.7	3545	10	BC074021	BC074021 Rattus no
10	541	93.1	3473	10	AY170344	AY170344 Mus muscu
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12	505.8	87.1	582	6	AX481423	AX481423 Sequence
13	505.8	87.1	582	9	HSU59747	U59747 Human Bcl-w
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16	501	86.2	583	6	AX022529	AX022529 Sequence
17	501	86.2	583	6	AX030817	AX030817 Sequence
18	497.4	85.6	579	6	AR020780	AR020780 Sequence
19	451.4	77.7	220818	2	AC128940	AC128940 Rattus no
20	451.4	77.7	223933	2	AC097389	AC097389 Rattus no
21	421.8	72.6	3815	10	BC040369	BC040369 Mus muscu
c 22	421.8	72.6	237561	10	AC116591	AC116591 Mus muscu
23	407.4	70.1	210784	2	AC119293	AC119293 Rattus no
24	407.4	70.1	263901	2	AC115371	AC115371 Rattus no
25	390.8	67.3	148278	2	AC079885	AC079885 Rattus no
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35	232.6	40.0	1053	5	BC073259	BC073259 Xenopus l
36	232.6	40.0	1894	5	BC084445	BC084445 Xenopus t
37	212.2	36.5	6049	6	AX345130	AX345130 Sequence
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39	142.4	24.5	1252	4	AB073983	AB073983 Canis fam
40	140.8	24.2	1163	4	AB080951	AB080951 Felis cat
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42	139.6	24.0	540	6	AX925690	AX925690 Sequence
43	139.4	24.0	600	6	AX925692	AX925692 Sequence
44	139.2	24.0	702	4	AY005131	AY005131 Oryctolag
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ALIGNMENTS

RESULT 1
AX022531
LOCUS AX022531 581 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 8 from Patent EP0932674.
ACCESSION AX022531
VERSION AX022531.1 GI:10046127
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes
JOURNAL Patent: EP 0932674-A 8 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
FEATURES Location/Qualifiers
source 1. .581
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CDS 1. .507
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AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
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ORIGIN

Query Match 100.0%; Score 581; DB 6; Length 581;
Best Local Similarity 100.0%; Pred. No. 9.9e-126;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
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Db        61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
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Qy       421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
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Qy       481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
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DEFINITION  Sequence 8 from Patent WO9735971.
ACCESSION   AX030819
VERSION     AX030819.1  GI:10278313
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
  TITLE     A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
            apoptosis-controlling genes
  JOURNAL   Patent: WO 9735971-A 8 02-OCT-1997;
            ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)
            ; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
FEATURES             Location/Qualifiers
     source          1. .581
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     CDS             1. .507
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  Query Match             100.0%;  Score 581;  DB 6;  Length 581;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-126;
  Matches  581;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
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Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
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Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
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RESULT 3
MMU59746

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LOCUS       MMU59746                582 bp    mRNA    linear   ROD 29-SEP-1996
DEFINITION  Mus musculus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION   U59746
VERSION     U59746.1  GI:1572494
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G.,
            Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
  TITLE     bcl-w, a novel member of the bcl-2 family, promotes cell survival
  JOURNAL   Oncogene 13 (4), 665-675 (1996)
  MEDLINE   96358615
   PUBMED   8761287
REFERENCE   2  (bases 1 to 582)
  AUTHORS   Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and
            Cory,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
            Eliza Hall Institute of Medical Research, PO Royal Melbourne
            Hospital, Parkville, Victoria 3050, Australia
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ORIGIN

  Query Match             96.4%;  Score 560.2;  DB 10;  Length 582;
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  Matches  568;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

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Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
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Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
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RESULT 4
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LOCUS       AF030769                3476 bp    mRNA    linear   ROD 16-NOV-1997
DEFINITION  Mus musculus BCL-W (Bcl-w) mRNA, complete cds.
ACCESSION   AF030769
VERSION     AF030769.1  GI:2623249
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3476)
  AUTHORS   Ross,A.J., Waymire,K.G., Moss,J.E., Parlow,A.F., Russell,L.D. and
            MacGregor,G.R.
  TITLE     Bcl-w is required for testis homeostasis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3476)
  AUTHORS   Ross,A.J. and MacGregor,G.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1997) Center for Molecular Medicine, Emory
            University, 1462 Clifton Road, Atlanta, GA 30322, USA
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                     /number=4
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ORIGIN

  Query Match             96.4%;  Score 560.2;  DB 10;  Length 3476;
  Best Local Similarity   97.8%;  Pred. No. 5.6e-121;
  Matches  568;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
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Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
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Db        299 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 358

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 418

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 478

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
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Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
Db        599 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 658

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
Db        659 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 718

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
Db        719 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 759
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RESULT 5
AK172925
LOCUS AK172925 3442 bp mRNA linear ROD 28-JUL-2004
DEFINITION Mus musculus mRNA for mKIAA0271 protein.
ACCESSION AK172925
VERSION AK172925.1 GI:50510434
KEYWORDS FLI_CDNA.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Okazaki,N., Kikuno,R.F., Ohara,R., Inamoto,S., Koseki,H., Hiraoka,S., Saga,Y., Seino,S., Nishimura,M., Kaisho,T., Hoshino,K., Kitamura,H., Nagase,T., Ohara,O. and Koga,H.
TITLE Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries
JOURNAL DNA Res. 11, 205-218 (2004)
REFERENCE 2 (bases 1 to 3442)
AUTHORS Okazaki,N., Kikuno,R.F., Nagase,T., Ohara,O. and Koga,H.
TITLE Direct Submission
JOURNAL Submitted (19-MAY-2004) Hisashi Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)
COMMENT The CREATE program supported by Japan science and technology corporation; cDNA full insert sequencing: Kazusa DNA Research Institute; cDNA library construction, clone selection and 5'- & 3'-end one pass sequencing.
FEATURES Location/Qualifiers
source 1. .3442
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="mia06063"
/note="vector:modified pBC SK+"
gene 1. .3442
/gene="mKIAA0271"
CDS <1. .581
/gene="mKIAA0271"
/note="CDS is predicted by in silico analysis. Start codon is not identified."
/codon_start=3
/evidence=not_experimental
/product="mKIAA0271 protein"
/protein_id="BAD32203.1"
/db_xref="GI:50510435"
/translation="RMATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLH QAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFV FGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEA
ORIGIN RRLREGNWASVRTVLTGAVALGALVTVGAFFC"

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Query Match
Best Local Similarity 94.5%; Score 549.2; DB 10; Length 3442;
Matches 557; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Db          6 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 65

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db         66 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 125

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db        126 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 185

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
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Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db        366 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 425

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
Db        426 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 485

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
Db        486 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 545

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTT 570
Db        546 GGGGCCCTGGTAACTGTAGGGGCCTTTTTT 575
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RESULT 6
AF096291
LOCUS AF096291 582 bp mRNA linear ROD 28-FEB-2000
DEFINITION Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION AF096291
VERSION AF096291.1 GI:3747129
KEYWORDS .
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 582)
AUTHORS Hamner,S., Skoglosa,Y. and Lindholm,D.
TITLE Differential expression of bcl-w and bcl-x messenger RNA in the developing and adult rat nervous system
JOURNAL Neuroscience 91 (2), 673-684 (1999)
MEDLINE 99292146
PUBMED 10366024
REFERENCE 2 (bases 1 to 582)
AUTHORS Hamner,S., Skoglosa,Y. and Lindholm,D.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala University, Box 587, BMC, Uppsala 751 23, Sweden
FEATURES Location/Qualifiers
source 1. .582
/organism="Rattus norvegicus"
/mol_type="mRNA"

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                     /db_xref="taxon:10116"
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                     /dev_stage="postnatal"
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CDS                  1. .582
                     /gene="bcl-w"
                     /note="Bcl-2 family member"
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                     /product="Bcl-w"
                     /protein_id="AAC64200.1"
                     /db_xref="GI:3747130"
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                     GAALCAESVNKEMEPLVGQVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEAR
                     RLREGNWASVRTVLTGAVALGALVTVGAFFASK"

ORIGIN

  Query Match          93.7%;  Score 544.2;  DB 10;  Length 582;
  Best Local Similarity  96.0%;  Pred. No. 4.2e-117;
  Matches  558;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
            1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db
Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
           61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120
Db
Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
           121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180
Db
Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
           181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db
Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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Db
Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
           301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360
Db
Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
           361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420
Db
Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
           421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACAGTGGTGACGGGGGCCGTGGCACTG 540
Db
Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
           481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 581
Db
Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
           541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
Db

RESULT 7
AY185100            1110 bp    mRNA    linear   ROD 24-JUN-2003
LOCUS       AY185100
DEFINITION  Rattus norvegicus BCL-WEL mRNA, complete cds.
ACCESSION   AY185100
VERSION     AY185100.1  GI:32185284
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 1110)
  AUTHORS   Itoh,T., Itoh,A. and Pleasure,D.
  TITLE     Bcl-2-related protein family gene expression during
            oligodendroglial differentiation
  JOURNAL   J. Neurochem. 85 (6), 1500-1512 (2003)
  MEDLINE   22672518
  PUBMED    12787069
REFERENCE   2  (bases 1 to 1110)
  AUTHORS   Itoh,T., Itoh,A. and Pleasure,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-2002) Neurology Research, The Children's Hospital
            of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center
            Blvd., Philadelphia, PA 19104, USA
FEATURES             Location/Qualifiers
     source          1. .1110
                     /organism="Rattus norvegicus"
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                     /strain="Sprague-Dawley"
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     CDS             431. .1090
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ORIGIN

  Query Match          93.7%;  Score 544.2;  DB 10;  Length 1110;
  Best Local Similarity  96.0%;  Pred. No. 3.8e-117;
  Matches  558;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
          509 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 568
Db
Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
          569 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 628
Db
Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
          629 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 688
Db
Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
          689 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 748
Db
Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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Db
Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
          809 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 868
Db
Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
          869 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 928
Db
Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
          929 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACAGTGGTGACGGGGGCCGTGGCACTG 988
Db
Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
          989 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 1048
Db
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Qy          541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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RESULT 8
AY185098
LOCUS       AY185098                 3487 bp    mRNA    linear   ROD 24-JUN-2003
DEFINITION  Rattus norvegicus BCL-W mRNA, complete cds.
ACCESSION   AY185098
VERSION     AY185098.1  GI:32185280
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 3487)
  AUTHORS   Itoh,T., Itoh,A. and Pleasure,D.
  TITLE     Bcl-2-related protein family gene expression during
            oligodendroglial differentiation
  JOURNAL   J. Neurochem. 85 (6), 1500-1512 (2003)
  MEDLINE   22672518
  PUBMED    12787069
REFERENCE   2  (bases 1 to 3487)
  AUTHORS   Itoh,T., Itoh,A. and Pleasure,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-2002) Neurology Research, The Children's Hospital
            of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center
            Blvd., Philadelphia, PA 19104, USA
FEATURES    Location/Qualifiers
     source 1. .3487
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ORIGIN

Query Match             93.7%;  Score 544.2;  DB 10;  Length 3487;
Best Local Similarity   96.0%;  Pred. No. 3.2e-117;
Matches  558;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db        170 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 229
Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db        230 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 289
Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db        290 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 349
Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        350 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 409
Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db        410 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 469
Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db        470 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 529
Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db        530 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 589
Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
Db        590 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 649
Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
Db        650 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 709
Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
Db        710 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 750

RESULT 9
BC074021
LOCUS       BC074021                 3545 bp    mRNA    linear   ROD 30-JUN-2004
DEFINITION  Rattus norvegicus cDNA clone MGC:91704 IMAGE:7105621, complete cds.
ACCESSION   BC074021
VERSION     BC074021.1  GI:49256646
KEYWORDS    MGC.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 3545)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED    12477932
REFERENCE   2  (bases 1 to 3545)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUN-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Howard Jacobs
            cDNA Library Preparation: Express Genomics
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 175 Row: p Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11177885.

FEATURES Location/Qualifiers
source 1. .3545
/organism="Rattus norvegicus"
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/db_xref="taxon:10116"
/clone="MGC:91704 IMAGE:7105621"
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CDS 199. .780
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/product="Unknown (protein for MGC:91704)"
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AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
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ORIGIN

Query Match 93.7%; Score 544.2; DB 10; Length 3545;
Best Local Similarity 96.0%; Pred. No. 3.2e-117;
Matches 558; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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Qy    1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db  199 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 258

Qy   61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db  259 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 318

Qy  121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db  319 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 378

Qy  181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db  379 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 438

Qy  241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db  439 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 498

Qy  301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db  499 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 558

Qy  361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db  559 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 618

Qy  421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
Db  619 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 678

Qy  481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
Db  679 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 738

Qy  541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
Db  739 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 779
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RESULT 10
AY170344
LOCUS AY170344 3473 bp mRNA linear ROD 27-JAN-2004
DEFINITION Mus musculus Bcl2-like protein 2 mRNA, complete cds.
ACCESSION AY170344
VERSION AY170344.2 GI:34857712
KEYWORDS .
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3473)
AUTHORS Su,H.-Y., Cheng,W.T.K., Chen,S.C., Lin,C.T., Lien,Y.Y., Liu,H.J. and Gilmour,R.S.
TITLE Mouse keratinocytes express c98, a novel gene homologous to bcl-2, that is stimulated by insulin-like growth factor 1 and prevents dexamethasone-induced apoptosis
JOURNAL Biochim. Biophys. Acta 1676 (2), 127-137 (2004)
REFERENCE 2 (bases 1 to 3473)
AUTHORS Su,H.-Y.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2002) Biotechnology, Pingtung University, No. 1, Hsueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan
REFERENCE 3 (bases 1 to 3473)
AUTHORS Su,H.-Y.
TITLE Direct Submission
JOURNAL Submitted (22-SEP-2003) Biotechnology, Pingtung University, No. 1, Hsueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan
REMARK Sequence update by submitter
COMMENT On Sep 22, 2003 this sequence version replaced gi:27497698.
FEATURES Location/Qualifiers
source 1. .3473
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/tissue_type="skin"
/dev_stage="neonatal"
/note="isolated after IGF-1 stimulation"
CDS 182. .763
/note="c98; Bcl2-c98"
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/product="Bcl2-like protein 2"
/protein_id="AAO13177.2"
/db_xref="GI:34857713"
/translation="MATPASTPDTRALVAYFVGYQLRQKGYVCGAGPGEGPAADPLHQ
AMRAAGDELQTRFRRTFSHLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKHMEPLVGQVQDWMVAYLETRLAYWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFAYK"

ORIGIN

Query Match 93.1%; Score 541; DB 10; Length 3473;
Best Local Similarity 95.7%; Pred. No. 1.8e-116;
Matches 556; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Qy    1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db  182 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTTACTTTGTAGGCTAT 241

Qy   61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db  242 CAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 301

Qy  121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db  302 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTGCAGACCCGTTTCCGCCGCACC 361
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Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        362 TTCTCTCACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 421

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db        422 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 481

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db        482 GTCTTTGGGGCTGCCCTGTGTGCAGAGAGTGTCAACAAACATATGGAGCCTTTGGTGGGA 541

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db        542 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTTACTGGATCCACAGC 601

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
Db        602 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 661

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
Db        662 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 721

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
Db        722 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTTACAAGTG 762
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RESULT 11
AR020779
LOCUS AR020779 579 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 1 from patent US 5789201.
ACCESSION AR020779
VERSION AR020779.1 GI:3975394
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 579)
AUTHORS Guastella,J.
TITLE Genes coding for bcl-y a bcl-2 homologue
JOURNAL Patent: US 5789201-A 1 04-AUG-1998;
FEATURES Location/Qualifiers
source 1. .579
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 93.0%; Score 540.6; DB 6; Length 579;
Best Local Similarity 95.9%; Pred. No. 3e-116;
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db         61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db        361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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RESULT 12
AX481423
LOCUS AX481423 582 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 37 from Patent WO02055693.
ACCESSION AX481423
VERSION AX481423.1 GI:22316337
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kreutzer,R., Limmer,S., Rost,S. and Hadwiger,P.
TITLE Method for inhibiting the expression of a target gene
JOURNAL Patent: WO 02055693-A 37 18-JUL-2002;
Ribopharma AG (DE)
FEATURES Location/Qualifiers
source 1. .582
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 87.1%; Score 505.8; DB 6; Length 582;
Best Local Similarity 91.9%; Pred. No. 4.3e-108;
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
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Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
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Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
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Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
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Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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RESULT 13
HSU59747
LOCUS HSU59747 582 bp mRNA linear PRI 29-SEP-1996
DEFINITION Human Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION U59747
VERSION U59747.1 GI:1572492
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G., Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
TITLE bcl-w, a novel member of the bcl-2 family, promotes cell survival
JOURNAL Oncogene 13 (4), 665-675 (1996)
MEDLINE 96358615
PUBMED 8761287
REFERENCE 2 (bases 1 to 582)
AUTHORS Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and Cory,S.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
FEATURES Location/Qualifiers
source 1. .582
/organism="Homo sapiens"
/mol_type="mRNA"
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gene 1. .582
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CDS 1. .582
/gene="bcl-w"
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/db_xref="GI:1572493"
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AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
ORIGIN

Query Match 87.1%; Score 505.8; DB 9; Length 582;
Best Local Similarity 91.9%; Pred. No. 4.3e-108;
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||||| ||||| ||||| |||||||||||| |||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
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Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||||||| |||||||| ||||| ||||||||| ||||| |||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||| |||||||||||||| |||||||||| |||||||||| ||||| || |||||||
Db        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
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Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
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Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
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Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
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Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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RESULT 14
D87461
LOCUS D87461 3542 bp mRNA linear PRI 10-JAN-2004
DEFINITION Homo sapiens mRNA for KIAA0271 gene, partial cds.
ACCESSION D87461
VERSION D87461.1 GI:1944417
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y., Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.
TITLE Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain
JOURNAL DNA Res. 3 (5), 321-329 (1996)
MEDLINE 97191544
PUBMED 9039502
REFERENCE 2 (bases 1 to 3542)
AUTHORS Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
FEATURES Location/Qualifiers
source 1. .3542
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HA6752"
/sex="male"
/cell_line="KG-1"
/cell_type="myloblast"
/tissue_type="brain"
/clone_lib="pSPORT 1"

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     CDS             <150. .758
                     /gene="KIAA0271"
                     /note="Start codon is not identified
                     similar to human transforming protein bcl-2 (A24428)"
                     /codon_start=1
                     /protein_id="BAA19666.2"
                     /db_xref="GI:40788933"
                     /translation="ELPSRLAARMATPASAPDTRALVADFVGYKLRQKGYVCGAGPGE
                     GPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNW
                     GRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALY
                     GDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK"
ORIGIN

  Query Match             86.5%;  Score 502.6;  DB 9;  Length 3542;
  Best Local Similarity   91.6%;  Pred. No. 1.8e-107;
  Matches  532;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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Db        177 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 236

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||| || |||||  ||||||||  || |||
Db        237 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 296

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||||||| ||||||||  |||||  ||||||||  |||||  ||||||
Db        297 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 356

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        357 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 416

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              |||||  |||||  ||||||||  ||||||||||  ||||||||||  |||||  ||  ||||||
Db        417 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 476

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||  ||||||||||||||||||||||  ||  |||||  ||  ||||||||
Db        477 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 536

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              |||||  |||||  |||||  ||||||||||||||||||  ||  ||||||||||||||||||||
Db        537 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 596

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              |||||  ||||||||||  ||||||||||||||||||||||||||||||||||||  ||  |||
Db        597 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 656

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||||  ||||||||||  ||||||  ||||||  ||||||||||||||||||||
Db        657 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 716

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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Db        717 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 757


RESULT 15
CQ730429
LOCUS       CQ730429                582 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 16363 from Patent WO02068579.
ACCESSION   CQ730429
VERSION     CQ730429.1  GI:42304244
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 16363 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .582
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match             86.2%;  Score 501;  DB 6;  Length 582;
  Best Local Similarity   91.4%;  Pred. No. 5.8e-107;
  Matches  531;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

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Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

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Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
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Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Perfect score: 581
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Gapop 10.0 , Gapext 1.0

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	581	100.0	581	2	AAT96578	Aat96578 Mouse bcl
2	581	100.0	581	2	AAX25135	Aax25135 Mouse bcl
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4	544.2	93.7	582	10	ADB52996	Adb52996 Primary r
5	540.6	93.0	579	2	AAV28333	Aav28333 Rat bcl-y
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8	505.8	87.1	582	6	ABZ35729	Abz35729 Human bcl
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10	505.8	87.1	582	6	ABL91694	Abl91694 Human pol
11	502.6	86.5	581	2	AAX25132	Aax25132 Human bcl
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22	364.4	62.7	1864	12	ADH73847	Adh73847 Human sec
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31	138.8	23.9	151	12	ACH93889	Ach93889 Human gen
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38	137.8	23.7	150	4	AAK39424	Aak39424 Human bon
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ALIGNMENTS

RESULT 1
AAT96578
ID AAT96578 standard; DNA; 581 BP.
XX
AC AAT96578;
XX
DT 22-APR-1998 (first entry)
XX
DE Mouse bcl-w DNA.
XX
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1. .507
FT /*tag= a
FT /product= "bcl-w"
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XX
PN WO9735971-A1.
XX
PD 02-OCT-1997.
XX
PF 27-MAR-1997; 97WO-AU000199.
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PR 27-MAR-1996; 96AU-00008965.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Cory S, Adams JM, Gibson LM, Holmgreen SP;
XX
DR WPI; 1997-489635/45.
DR P-PSDB; AAW36048.
XX
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
PT inhibit cell survival, e.g. for treatment of cancer and degenerative
PT diseases.
XX
PS Claim 3; Page 50-51; 86pp; English.
XX
CC This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene

CC family. This gene promotes cell survival, so its modulation is useful in
CC treatment of cancer or auto-immune diseases, degenerative diseases (e.g.
CC stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,
CC hypoxia, ischaemia, human immunodeficiency virus infection or in cell
CC transplants. Up-regulation of the gene can also be used to modify cell
CC lines cultured in vivo, e.g. to develop new lines, to facilitate
CC isolation of hybridomas and to increase survival of primary explants
CC during genetic modification. It can be used to produce recombinant Bcl-w
CC for therapy, diagnosis, antibody production or screening of potential
CC modulators
XX
SQ Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 U; 0 Other;

Query Match 100.0%; Score 581; DB 2; Length 581;
Best Local Similarity 100.0%; Pred. No. 8.4e-148;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
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Qy  181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy  241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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RESULT 2
AAX25135
ID AAX25135 standard; DNA; 581 BP.
XX
AC AAX25135;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse bcl-w gene derivative.
XX
KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
KW animal model; ss.
XX
OS Mus sp.
XX

FH Key Location/Qualifiers
FT CDS 1. .507
FT /*tag= a
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
DR WPI; 1999-243890/20.
DR P-PSDB; AAY05533.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w.
XX
PS Disclosure; Page 38; 52pp; English.
XX
CC The present sequence is described as a derivative of the mouse bcl-w gene
CC (see AAX25133) and encodes Bcl-w protein (see AAY05533), a pro-survival
CC member of the Bcl-2 family which is widely expressed and which is
CC essential for spermatogenesis. The invention relates generally to a
CC method of treatment and to an animal model for the identification of
CC molecules and genetic sequences useful for inducing or reducing fertility
CC of male animals. Methods are provided for the treatment of infertility,
CC or for reducing fertility, by modulating spermatogenesis. An animal model
CC carries a mutation is at least one allele of the human or murine bcl-w
CC gene or in a gene associated with bcl-w. Such animals have disorganised
CC seminferous tubules and are substantially infertile, but possess no other
CC major abnormalities as determined by histological examination. They can
CC be used to screen for therapeutic molecules including genetic sequences
CC capable of inducing, enhancing or otherwise facilitating spermatogenesis
CC in animals, or which can induce infertility
XX
SQ Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 U; 0 Other;

Query Match 100.0%; Score 581; DB 2; Length 581;
Best Local Similarity 100.0%; Pred. No. 8.4e-148;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
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Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
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RESULT 3
AAX25133
ID AAX25133 standard; DNA; 581 BP.
XX
AC AAX25133;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse bcl-w gene.
XX
KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
KW animal model; ss.
XX
OS Mus sp.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
DR WPI; 1999-243890/20.
DR P-PSDB; AAY05531.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w.
XX
PS Claim 3; Page 34; 52pp; English.
XX
CC The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see
CC AAY05531), a pro-survival member of the Bcl-2 family which is widely
CC expressed and which is essential for spermatogenesis. The invention
CC relates generally to a method of treatment and to an animal model for the
CC identification of molecules and genetic sequences useful for inducing or
CC reducing fertility of male animals. Methods are provided for the
CC treatment of infertility, or for reducing fertility, by modulating
CC spermatogenesis. An animal model carries a mutation is at least one
CC allele of the human or murine bcl-w gene or in a gene associated with bcl
CC -w. Such animals have disorganised seminferous tubules and are
CC substantially infertile, but possess no other major abnormalities as
CC determined by histological examination. They can be used to screen for
CC therapeutic molecules including genetic sequences capable of inducing,
CC enhancing or otherwise facilitating spermatogenesis in animals, or which
CC can induce infertility
XX
SQ Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 U; 0 Other;

Query Match 96.4%; Score 560.2; DB 2; Length 581;
Best Local Similarity 97.8%; Pred. No. 3.8e-142;
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Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
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Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
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Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
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RESULT 4
ADB52996
ID ADB52996 standard; DNA; 582 BP.
XX
AC ADB52996;
XX
DT 04-DEC-2003 (first entry)
XX
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3538.
XX
KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
KW primary rat hepatocyte toxicity modelling; gene; ds.
XX
OS Rattus norvegicus.
XX
PN WO2003065993-A2.
XX
PD 14-AUG-2003.
XX
PF 04-FEB-2003; 2003WO-US003482.
XX
PR 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-0363534P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371150P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
PR 19-APR-2002; 2002US-0373602P.
PR 22-APR-2002; 2002US-0374139P.
PR 08-MAY-2002; 2002US-0378370P.
PR 09-MAY-2002; 2002US-0378652P.

PR 09-MAY-2002; 2002US-0378653P.
PR 09-MAY-2002; 2002US-0378665P.
PR 09-JUL-2002; 2002US-0394230P.
PR 09-JUL-2002; 2002US-0394253P.
PR 04-SEP-2002; 2002US-0407688P.
PR 28-JAN-2003; 2003US-0442900P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
PI Elashoff M;
XX
DR WPI; 2003-731472/69.
XX
PT Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT mean values.
XX
PS Claim 44; SEQ ID NO 3538; 874pp; English.
XX
CC The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
XX
SQ Sequence 582 BP; 111 A; 157 C; 200 G; 114 T; 0 U; 0 Other;

Query Match 93.7%; Score 544.2; DB 10; Length 582;
Best Local Similarity 96.0%; Pred. No. 8.5e-138;
Matches 558; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

```
Qy        1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
            ||| ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy       61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
            | |||||||||||||||||||||||||||||||||| |||||||||||||||| ||||||
Db       61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy      121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
            |||||||||||||||||||||| |||||||||||||||||||||| ||||| ||||||
Db      121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy      181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy      241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
            |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db      241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy      301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
            |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db      301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy      361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
            ||||| |||||||||| ||| |||||||||||||||  ||||||||||||||||||||||
Db      361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy      421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
            ||||| |||||||||| |||||||||||||||||||||||||||||||| ||||||||||
Db      421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480
```

Qy 481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
Db 481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy 541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
Db 541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581

RESULT 5
AAV28333
ID AAV28333 standard; cDNA; 579 BP.
XX
AC AAV28333;
XX
DT 02-OCT-1998 (first entry)
XX
DE Rat bcl-y gene.
XX
KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT CDS 1. .579
FT /*tag= a
FT /product= "bcl-y"
FT /note= "No stop codon given"
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97US-00798897.
XX
PR 23-FEB-1996; 96US-0012201P.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1998-446079/38.
DR P-PSDB; AAW61391.
XX
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
PT recombinant protein for use in treating uncontrolled cell growth e.g.
PT cancers.
XX
PS Claim 2; Column 13/14; 27pp; English.
XX
CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2
CC family, components in the cell death pathway. The bcl-2 family have both
CC apoptotic activity and the apoptosis blocking activity. bcl-y falls in
CC the apoptosis activity category. The recombinant protein may be used to
CC prevent uncontrolled cell growth, either by its direct administration to
CC recombinant genetic constructs to increase its expression in vivo. Also,
CC antisense constructs can be used in disorders where prevention of cell
CC death is desired
XX
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;

Query Match 93.0%; Score 540.6; DB 2; Length 579;
Best Local Similarity 95.9%; Pred. No. 8e-137;
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

```
Qy        1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
            ||| ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy       61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
            | |||||| |||||||||||||||||||||||| |||||||||||||||| ||||||
Db       61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120
```

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Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              ||||||||||||||||||||||| |||||||||||||||||||||||| ||||| ||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| |||||||||||| ||| |||||||||||||||  ||||||||||||||||||||
Db        361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              ||||| |||||||||||| |||||||||||||||||||||||||||||||||| ||||||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||||| |||||||||| |||||| |||||| |||||||||| |||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
              |||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
```

RESULT 6
AAX15945
ID AAX15945 standard; cDNA; 579 BP.
XX
AC AAX15945;
XX
DT 20-MAY-1999 (first entry)
XX
DE cDNA encoding the rat bcl-y protein.
XX
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite;
KW ss.
XX
OS Rattus sp.
XX
PN US5883229-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-00978523.
XX
PR 23-FEB-1996; 96US-0012201P.
PR 11-FEB-1997; 97US-00798897.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1999-214150/18.
DR P-PSDB; AAW97391.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT modulating programmed cell death.
XX
PS Disclosure; Col 13-16; 26pp; English.
XX
CC The present sequence encodes rat bcl-y protein (Rbcl-y). The
CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC - conditions where cells under go premature cell death as a result of
CC triggers which may or may not be apparent. They may also be used in this
CC way to develop cell lines which remain viable in culture for an extended
CC period. In contrast, if they act as cell death stimulators, Rbcl-y and
CC Hbcl-y may be used to treat conditions associated with prolonged cell
CC life span such as cancer (especially kaposi's sarcoma and lung cancer)
CC and auto/hyperimmune diseases. They may also be used to cause cell death
CC in, and hence control, parasites
XX
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;

Query Match 93.0%; Score 540.6; DB 2; Length 579;
Best Local Similarity 95.9%; Pred. No. 8e-137;
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

```
Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||| |||||||||||||||||||||||| |||||||||||||||| ||||||
Db         61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              ||||||||||||||||||||||| |||||||||||||||||||||||| ||||| ||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| |||||||||||| ||| |||||||||||||||  ||||||||||||||||||||
Db        361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              ||||| |||||||||||| |||||||||||||||||||||||||||||||||| ||||||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||||| |||||||||| |||||| |||||| |||||||||| |||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
              |||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
```

RESULT 7
ABV78153
ID ABV78153 standard; DNA; 582 BP.
XX

AC ABV78153;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human bcl-w DNA SEQ ID NO 37.
XX
KW RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;
KW virucide; protozoacide; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200255693-A2.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2002; 2002WO-EP000152.
XX
PR 09-JAN-2001; 2001DE-01000586.
PR 26-OCT-2001; 2001DE-01055280.
PR 29-NOV-2001; 2001DE-01058411.
PR 07-DEC-2001; 2001DE-01060151.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
DR WPI; 2002-590671/63.
XX
PT Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
PT target and having an overhang.
XX
PS Claim 10; Page 134; 203pp; German.
XX
CC The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in Plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a gene related to the invention
XX
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 87.1%; Score 505.8; DB 6; Length 582;
Best Local Similarity 91.9%; Pred. No. 2.3e-127;
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

```
Qy    1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db    1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy   61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db   61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy  121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db  121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy  181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db  181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy  241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db  241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
```

Qy 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy 361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db 361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy 421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
Db 421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy 481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
Db 481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy 541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
Db 541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581

RESULT 8
ABZ35729
ID ABZ35729 standard; DNA; 582 BP.
XX
AC ABZ35729;
XX
DT 07-FEB-2003 (first entry)
XX
DE Human bcl-w polynucleotide SEQ ID NO 37.
XX
KW Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;
KW protozoacide; gene expression; antisense; tumour; infection; Plasmodium;
KW virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
KW Hepatitis C virus; human papilloma virus; gene; ds.
XX
OS Homo sapiens.
XX
PN DE10100588-A1.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2001; 2001DE-01000588.
XX
PR 09-JAN-2001; 2001DE-01000588.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
DR WPI; 2002-683450/74.
XX
PT Inhibiting expression of target genes, useful e.g. for treating tumors,
PT by introducing into cells two double-stranded RNAs that are complementary
PT to the target.
XX
PS Claim 13; Page 30-31; 100pp; German.
XX
CC The invention relates to inhibiting expression of a target gene in a cell
CC by introducing at least two oligoribonucleotides (dsRNAI and II), both
CC with a double-stranded (ds) structure of at most 49 sequential nucleotide
CC pairs. At least part of one strand (S1, S2) of the ds structures in each
CC of dsRNAI and II are complementary to regions in the target gene. The
CC method uses antisense inhibition of gene expression using double stranded
CC RNA inhibition (RNAi). The method is particularly used to treat tumours
CC or infections, especially by Plasmodium or viruses/viroids (pathogenic on
CC humans, animals or plants). The method provides more effective inhibition
CC of expression than known methods using a single dsRNA, even at very low
CC concentrations. When dsRNA has at least one unpaired nucleotide at the
CC end, stability (and thus effective concentration in the cell) is improved
CC and efficiency can be increased further by pretreating the cells with
CC interferon. The present sequence is that of a target DNA of the invention
XX

```
SQ   Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

  Query Match             87.1%;  Score 505.8;  DB 6;  Length 582;
  Best Local Similarity   91.9%;  Pred. No. 2.3e-127;
  Matches  534;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||| ||||| ||||| |||||||||||| |||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||| |||||||||||||| |||||||||| |||||||||| ||||| || ||||||
Db        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||||| || ||||| ||  ||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| ||||| |||||||||||||||| || ||||||||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              ||||| |||||||||||| |||||||||||||||||||||||||||||||||| || |||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||||| |||||||||| |||||| |||||| ||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
              |||||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT 9
ABX09972
ID   ABX09972 standard; DNA; 582 BP.
XX
AC   ABX09972;
XX
DT   23-JAN-2003  (first entry)
XX
DE   Human bcl-w DNA fragment SEQ ID 37.
XX
KW   Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;
KW   prion; inhibition; human; ds.
XX
OS   Homo sapiens.
XX
PN   DE10100587-C1.
XX
PD   21-NOV-2002.
XX
PF   09-JAN-2001; 2001DE-01000587.
XX
PR   09-JAN-2001; 2001DE-01000587.
XX
PA   (RIBO-) RIBOPHARMA AG.
XX
PI   Kreutzer R,  Limmer S,  Rost S,  Hadwiger P;
XX
DR   WPI; 2002-742209/81.
XX
PT   Inhibiting expression of target genes, e.g. oncogenes, in cells, by
PT   introduction of complementary double-stranded oligoribonucleotide, after
PT   treating the cell with interferon.
XX
PS   Disclosure; Page 35-36; 98pp; German.
XX
CC   This invention describes a novel method for inhibiting expression of a
CC   target gene by introducing into the cell that contains the target gene at
CC   least one oligoribonucleotide (dsRNAI) that has a double-stranded (ds)
CC   structure of not more than 49 consecutive nucleotides (nt), where at
CC   least a segment of one strand of the ds structure is complementary with
CC   the target gene and the cells are treated with interferon before
CC   introduction of dsRNAI. The method is used to inhibit expression of
CC   target genes, particularly oncogenes, cytokine genes, Id (not defined)
CC   protein genes; developmental or prion genes, or genes expressed in
CC   pathogenic organisms (particularly plasmodia) or in viruses or viroids
CC   (pathogenic in humans, animals or plants). Treating the cells with
CC   interferon greatly increases the extent to which dsRNA can inhibit
CC   expression of the target genes, and the effect is even greater when dsRNA
CC   are modified to increase their stability. ABX09936-ABX10075 represent
CC   gene fragments used to illustrate the method of the invention
XX
SQ   Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

  Query Match             87.1%;  Score 505.8;  DB 6;  Length 582;
  Best Local Similarity   91.9%;  Pred. No. 2.3e-127;
  Matches  534;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||| ||||| ||||| |||||||||||| |||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||| |||||||||||||| |||||||||| |||||||||| ||||| || ||||||
Db        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||||| || ||||| ||  ||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| ||||| |||||||||||||||| || ||||||||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              ||||| |||||||||||| |||||||||||||||||||||||||||||||||| || |||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||||| |||||||||| |||||| |||||| ||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
              |||||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT 10
```

```
ABL91694
ID   ABL91694 standard; DNA; 582 BP.
XX
AC   ABL91694;
XX
DT   28-MAY-2002  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 37.
XX
KW   Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
KW   Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
KW   cytostatic; virucide; protozoacide; antibacterial; ds.
XX
OS   Homo sapiens.
XX
PN   DE10100586-C1.
XX
PD   11-APR-2002.
XX
PF   09-JAN-2001; 2001DE-01000586.
XX
PR   09-JAN-2001; 2001DE-01000586.
XX
PA   (RIBO-) RIBOPHARMA AG.
XX
PI   Kreutzer R,  Limmer S,  Rost S,  Hadwiger P;
XX
DR   WPI; 2002-270454/32.
XX
PT   Inhibiting gene expression in cells, useful for e.g. treating tumors, by
PT   introducing double-stranded complementary oligoRNA having unpaired
PT   terminal bases.
XX
PS   Claim 13; Page 32; 104pp; German.
XX
CC   The invention relates to a method for inhibiting expression of a target
CC   gene (ABL91658-ABL91797) in a cell by introducing at least one
CC   oligoribonucleotide that has a double-stranded structure consisting of at
CC   most 49 sequential nucleotide pairs, with at least part of one strand
CC   complementary with the target gene and has at least one end a single-
CC   stranded segment of 1-4 nt. The method provides oligoribonucleotides for
CC   antisense inhibition of gene expression useful e.g. for treating tumours
CC   but the oligoribonucleotides may also be directed against genes present
CC   in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans,
CC   animals or plants) or against cytokine, Id, developmental or prion genes.
CC   The method provides more effective inhibition of gene expression than use
CC   of known oligonucleotides, probably because the unpaired overhang
CC   increases stability and thus intracellular concentration
XX
SQ   Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

  Query Match             87.1%;  Score 505.8;  DB 6;  Length 582;
  Best Local Similarity   91.9%;  Pred. No. 2.3e-127;
  Matches  534;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||| ||||| ||||| |||||||||||| |||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||||| |||||||| ||||| |||||||| ||||| |||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||| |||||||||||||| |||||||||| |||||||||| ||||| || ||||||

Db        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||||||||| || |||||| ||  |||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              |||||  |||||  |||||  |||||||||||||||||| || ||||||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              |||||  |||||||||||| ||||||||||||||||||||||||||||||||||| ||| |
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||||| |||||||||| |||||| |||||| ||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
              |||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
```

```
RESULT 11
AAX25132
ID   AAX25132 standard; DNA; 581 BP.
XX
AC   AAX25132;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Human bcl-w gene.
XX
KW   Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
KW   animal model; ss.
XX
OS   Homo sapiens.
XX
PN   WO9913710-A1.
XX
PD   25-MAR-1999.
XX
PF   16-SEP-1998;   98WO-AU000764.
XX
PR   16-SEP-1997;   97AU-00009228.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Cory S,  Adams J,  Print C,  Gibson L,  Koentgen F;
XX
DR   WPI; 1999-243890/20.
DR   P-PSDB; AAY05530.
XX
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w.
XX
PS   Claim 3; Page 32; 52pp; English.
XX
CC   The present sequence is the human bcl-w gene encoding Bcl-w protein (see
CC   AAY05530), a pro-survival member of the Bcl-2 family which is widely
CC   expressed and which is essential for spermatogenesis. The invention
CC   relates generally to a method of treatment and to an animal model for the
CC   identification of molecules and genetic sequences useful for inducing or
CC   reducing fertility of male animals. Methods are provided for the
CC   treatment of infertility, or for reducing fertility, by modulating
CC   spermatogenesis. An animal model carries a mutation is at least one
CC   allele of the human or murine bcl-w gene or in a gene associated with bcl
CC   -w. Such animals have disorganised seminferous tubules and are
CC   substantially infertile, but possess no other major abnormalities as
CC   determined by histological examination. They can be used to screen for
CC   therapeutic molecules including genetic sequences capable of inducing,
CC   enhancing or otherwise facilitating spermatogenesis in animals, or which
CC   can induce infertility
```

```
XX
SQ   Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 U; 0 Other;

  Query Match            86.5%;  Score 502.6;  DB 2;  Length 581;
  Best Local Similarity  91.6%;  Pred. No. 1.7e-126;
  Matches  532;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||| ||||| ||||| |||||||||||| |||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || |||||||||||||||||||| ||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||| ||||| |||||||| |||||||||| |||||||||| ||||| || ||||||
Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||||||| || ||||| ||  ||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| ||||| |||||||||||||||| || |||||||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              ||||| |||||||||||| |||||||||||||||||||||||||||||||||| || |||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||||| |||||||||| ||||||| |||||||| |||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
              |||||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT 12
ABT16642
ID   ABT16642 standard; DNA; 3542 BP.
XX
AC   ABT16642;
XX
DT   03-APR-2003  (first entry)
XX
DE   Human bcl-2 gene SEQ ID No 4.
XX
KW   Anti-tumour; DNAzyme; bcl-2 gene; tumour; malignant; chemotherapy;
KW   radiation therapy; catalytic domain; enzyme; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO200299090-A1.
XX
PD   12-DEC-2002.
XX
PF   07-JUN-2002; 2002WO-AU000739.
XX
PR   07-JUN-2001; 2001AU-00005527.
XX
PA   (JOHJ ) JOHNSON & JOHNSON RES PTY LTD.
XX
PI   Sun L,  Wang L,  Turner RJ,  Saravolac EG,  Dass CR;
XX
DR   WPI; 2003-140617/13.
XX
PT   Novel DNAzyme useful for treating tumors, and for enhancing the
PT   sensitivity of malignant or virus infected cells to therapy, comprises a
PT   catalytic domain and binding domain contiguous to the catalytic domain.
XX
PS   Disclosure; Page 44-45; 67pp; English.
XX
CC   The invention relates to a DNAzyme which specifically cleaves mRNA
CC   transcribed from a member of the bcl-2 gene family. The DNAzymes comprise
CC   a catalytic domain, binding domains contiguous with the 5' and 3' end of
CC   the catalytic domain, and therefore hybridise with, the two regions
CC   immediately flanking the purine residue of the cleavage site within the
CC   bcl-2 gene family mRNA, at which DNAzyme-catalysed cleavage is desired. A
CC   pharmaceutical composition comprising a DNAzyme of the invention is
CC   useful for treating tumours in a subject, and for enhancing the
CC   sensitivity of malignant or virus infected cells infected cells to
CC   therapy. The DNAzymes are useful in diagnostics, therapeutics,
CC   prophylaxis, research agents and in kits. The DNAzymes are also useful
CC   for increasing the susceptibility of tumour cells to anti-tumour
CC   therapies such as chemotherapy and radiation therapy. This polynucleotide
CC   sequence represents a human bcl-2 gene of the invention
XX
SQ   Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 U; 0 Other;

  Query Match            86.5%;  Score 502.6;  DB 8;  Length 3542;
  Best Local Similarity  91.6%;  Pred. No. 3e-126;
  Matches  532;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||| ||||| ||||| |||||||||||| |||
Db        177 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 236

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db        237 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 296

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        297 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 356

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || |||||||||||||||||||| ||||||||||||
Db        357 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 416

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||| ||||| |||||||| |||||||||| |||||||||| ||||| || ||||||
Db        417 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 476

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||||||| || ||||| ||  ||||||||
Db        477 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 536

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| ||||| |||||||||||||||| || |||||||||||||||||||||
Db        537 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 596

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              ||||| |||||||||||| |||||||||||||||||||||||||||||||||| || |||
Db        597 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 656

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||||| |||||||||| ||||||| |||||||| |||||||||||||||||
Db        657 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 716

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
              |||||||||||||||||||||||||||||||||||||||||
Db        717 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 757


RESULT 13
```

AAT96577
ID AAT96577 standard; DNA; 583 BP.
XX
AC AAT96577;
XX
DT 22-APR-1998 (first entry)
XX
DE Human bcl-w DNA.
XX
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .582
FT /*tag= a
FT /product= "bcl-w"
XX
PN WO9735971-A1.
XX
PD 02-OCT-1997.
XX
PF 27-MAR-1997; 97WO-AU000199.
XX
PR 27-MAR-1996; 96AU-00008965.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Cory S, Adams JM, Gibson LM, Holmgreen SP;
XX
DR WPI; 1997-489635/45.
DR P-PSDB; AAW36047.
XX
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
PT inhibit cell survival, e.g. for treatment of cancer and degenerative
PT diseases.
XX
PS Claim 3; Page 48; 86pp; English.
XX
CC This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
CC family, extracted from an adult brain library. This gene promotes cell
CC survival, so its modulation is useful in treatment of cancer or auto-
CC immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease,
CC myocardial infarct, muscular degeneration, hypoxia, ischaemia, human
CC immunodeficiency virus infection or in cell transplants. Up-regulation of
CC the gene can also be used to modify cell lines cultured in vivo, e.g. to
CC develop new lines, to facilitate isolation of hybridomas and to increase
CC survival of primary explants during genetic modification. It can be used
CC to produce recombinant Bcl-w for therapy, diagnosis, antibody production
CC or screening of potential modulators
XX
SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;

Query Match 86.2%; Score 501; DB 2; Length 583;
Best Local Similarity 91.4%; Pred. No. 4.7e-126;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

```
Qy    1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db    1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy   61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db   61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy  121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db  121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy  181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db  181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy  241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db  241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy  301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db  301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy  361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db  361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420

Qy  421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
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Qy  481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
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Qy  541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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```

RESULT 14
AAX25134
ID AAX25134 standard; DNA; 583 BP.
XX
AC AAX25134;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human bcl-w gene derivative.
XX
KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
KW animal model; ss.
XX
OS Homo sapiens.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
DR WPI; 1999-243890/20.
DR P-PSDB; AAY05532.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w.
XX
PS Disclosure; Page 36; 52pp; English.
XX
CC The present sequence is described as a derivative of the human bcl-w gene
CC (see AAX25132) and encodes Bcl-w protein (see AAY05532), a pro-survival
CC member of the Bcl-2 family which is widely expressed and which is
CC essential for spermatogenesis. The invention relates generally to a
CC method of treatment and to an animal model for the identification of
CC molecules and genetic sequences useful for inducing or reducing fertility
CC of male animals. Methods are provided for the treatment of infertility,
CC or for reducing fertility, by modulating spermatogenesis. An animal model
CC carries a mutation is at least one allele of the human or murine bcl-w
CC gene or in a gene associated with bcl-w. Such animals have disorganised
CC seminferous tubules and are substantially infertile, but possess no other
CC major abnormalities as determined by histological examination. They can

```
CC   be used to screen for therapeutic molecules including genetic sequences
CC   capable of inducing, enhancing or otherwise facilitating spermatogenesis
CC   in animals, or which can induce infertility
XX
SQ   Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;

  Query Match             86.2%;  Score 501;  DB 2;  Length 583;
  Best Local Similarity   91.4%;  Pred. No. 4.7e-126;
  Matches  531;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||| ||||| ||||| |||||||||| |||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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Db        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||| || ||||| ||   ||||||||
Db        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| |||||||||||||||||||| || |||| ||||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
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RESULT 15
AAV28334
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XX
AC   AAV28334;
XX
DT   02-OCT-1998  (first entry)
XX
DE   Human bcl-y gene.
XX
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XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .579
FT                   /*tag=  a
FT                   /product= "bcl-y"
FT                   /note= "No stop codon given"
XX
PN   US5789201-A.
XX
PD   04-AUG-1998.
XX
PF   11-FEB-1997;   97US-00798897.
XX
PR   23-FEB-1996;   96US-0012201P.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1998-446079/38.
DR   P-PSDB; AAW61392.
XX
PT   Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
PT   recombinant protein for use in treating uncontrolled cell growth e.g.
PT   cancers.
XX
PS   Claim 3; Column 15/16; 27pp; English.
XX
CC   The mammalian bcl-y genes encode a protein that is a member of the bcl-2
CC   family, components in the cell death pathway. The bcl-2 family have both
CC   apoptotic activity and the apoptosis blocking activity. bcl-y falls in
CC   the apoptosis activity category. The recombinant protein may be used to
CC   prevent uncontrolled cell growth, either by its direct administration to
CC   recombinant genetic constructs to increase its expression in vivo. Also,
CC   antisense constructs can be used in disorders where prevention of cell
CC   death is desired
XX
SQ   Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;

  Query Match             85.6%;  Score 497.4;  DB 2;  Length 579;
  Best Local Similarity   91.2%;  Pred. No. 4.5e-125;
  Matches  528;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||| ||||| ||||  |||||||||| |||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              || |||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || |||||||||||||||||||| ||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||| ||||| |||||||| |||||||||| ||||| || ||||||
Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||| || ||||| ||  ||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| |||||||||||||||||| || ||||||||||||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              ||||| |||||||||||| |||||||||||||||||||||||||||||||||| || |||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
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Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

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Job time : 457.215 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 16:31:16 ; Search time 143.753 Seconds
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Title: US-09-925-674B-8
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	581	100.0	581	4	US-09-155-327G-8	Sequence 8, Appli
2	540.6	93.0	579	1	US-08-798-897-1	Sequence 1, Appli
3	540.6	93.0	579	2	US-08-978-523-1	Sequence 1, Appli
4	501	86.2	582	4	US-09-949-016-5057	Sequence 5057, Ap
5	501	86.2	583	4	US-09-155-327G-6	Sequence 6, Appli
6	497.4	85.6	579	1	US-08-798-897-2	Sequence 2, Appli
7	497.4	85.6	579	2	US-08-978-523-2	Sequence 2, Appli
8	364.8	62.8	1098	4	US-09-010-147B-23	Sequence 23, Appl
9	364.4	62.7	1864	3	US-09-149-476-130	Sequence 130, App
10	364.2	62.7	5199	4	US-09-949-016-16799	Sequence 16799, A
11	357	61.4	601	4	US-09-949-016-177003	Sequence 177003,
12	134.6	23.2	926	1	US-08-081-448-5	Sequence 5, Appli
13	134.6	23.2	926	2	US-08-470-670A-6	Sequence 6, Appli
14	134.6	23.2	926	3	US-08-481-739-1	Sequence 1, Appli
15	134.6	23.2	926	3	US-09-167-921-1	Sequence 1, Appli
16	134.6	23.2	926	3	US-09-277-020-39	Sequence 39, Appl
17	134.6	23.2	926	3	US-09-323-743-1	Sequence 1, Appli
18	134.6	23.2	926	3	US-08-461-511A-6	Sequence 6, Appli
19	134.6	23.2	926	3	US-09-271-014A-5	Sequence 5, Appli
20	134.6	23.2	926	4	US-09-023-655-1430	Sequence 1430, Ap
21	134.6	23.2	926	4	US-09-814-915A-106	Sequence 106, App
22	134.6	23.2	926	5	PCT-US94-07089-6	Sequence 6, Appli
23	134.6	23.2	1236	4	US-09-639-245-1	Sequence 1, Appli
24	130.6	22.5	1455	4	US-09-639-245-7	Sequence 7, Appli
25	126.8	21.8	60489	4	US-09-949-016-16287	Sequence 16287, A
26	125	21.5	717	2	US-08-465-485A-20	Sequence 20, Appl
27	125	21.5	717	3	US-09-080-285-20	Sequence 20, Appl
28	125	21.5	4825	6	5459251-1	Patent No. 5459251
29	125	21.5	4825	6	5459251-1	Patent No. 5459251
30	125	21.5	5086	2	US-08-465-485A-19	Sequence 19, Appl
31	125	21.5	5086	2	US-08-365-486A-14	Sequence 14, Appl
32	125	21.5	5086	3	US-09-080-285-19	Sequence 19, Appl
33	125	21.5	5086	3	US-08-880-342-14	Sequence 14, Appl
34	125	21.5	5086	3	US-09-724-426-19	Sequence 19, Appl
35	125	21.5	5086	3	US-09-233-527-7	Sequence 7, Appli
36	125	21.5	5086	5	PCT-US93-05651-4	Sequence 4, Appli
37	125	21.5	5086	5	PCT-US93-06251-2	Sequence 2, Appli
38	125	21.5	5094	3	US-09-234-186-7	Sequence 7, Appli
39	125	21.5	5104	6	5506344-1	Patent No. 5506344
40	125	21.5	5104	6	5506344-1	Patent No. 5506344
41	125	21.5	6030	4	US-09-023-655-1015	Sequence 1015, Ap
42	123.4	21.2	760	1	US-08-405-702A-11	Sequence 11, Appl
43	123.4	21.2	1846	2	US-08-365-486A-16	Sequence 16, Appl
44	123.4	21.2	1846	3	US-08-880-342-16	Sequence 16, Appl
45	121.8	21.0	711	4	US-09-741-238-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-155-327G-8
; Sequence 8, Application US/09155327G
; Patent No. 6790637
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 2096584
; CURRENT APPLICATION NUMBER: US/09/155,327G
; CURRENT FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(579)
US-09-155-327G-8

Query Match 100.0%; Score 581; DB 4; Length 581;
Best Local Similarity 100.0%; Pred. No. 7.5e-162;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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RESULT 2
US-08-798-897-1
; Sequence 1, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-08-798-897-1

Query Match 93.0%; Score 540.6; DB 1; Length 579;
Best Local Similarity 95.9%; Pred. No. 6.6e-150;
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||| |||||||||||||||||||||||| |||||||||||||||| ||||||
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Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
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Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| |||||||||||| ||| |||||||||||||||  ||||||||||||||||||||
Db        361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
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Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||||| |||||||||| |||||| |||||| |||||||||| ||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
              |||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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RESULT 3
US-08-978-523-1
; Sequence 1, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both

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;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-978-523-1

  Query Match             93.0%;  Score 540.6;  DB 2;  Length 579;
  Best Local Similarity   95.9%;  Pred. No. 6.6e-150;
  Matches  555;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||| |||||||||||||||||||||||||| |||||||||||||||||| ||||||
Db         61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||| |||||||||||||||||||| ||||| ||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| |||||||||||| ||| |||||||||||||||  ||||||||||||||||||||
Db        361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              ||||| |||||||||||| |||||||||||||||||||||||||||||||||| ||||||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||||| |||||||||| |||||| |||||| |||||||||| |||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
              |||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579


RESULT 4
US-09-949-016-5057
; Sequence 5057, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5057
;   LENGTH: 582
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5057

  Query Match             86.2%;  Score 501;  DB 4;  Length 582;
  Best Local Similarity   91.4%;  Pred. No. 3.4e-138;
  Matches  531;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||||  ||||| ||||| ||||||||||| |||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              || |||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| |||||| |||||||| || |||||||||||||||||||| ||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||| ||||| |||||||| |||||||||| |||||||||| ||||| || ||||||
Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||||||||||||||||||||||||||||||||| || ||||| ||  ||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| |||||||||||||||||| || ||||||||||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              ||||| |||||||||| ||||||||||||||||||||||||||||||||||||| || |||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||||| |||||||||| |||||| |||||| ||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
              |||||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT 5
US-09-155-327G-6
; Sequence 6, Application US/09155327G
; Patent No. 6790637
; GENERAL INFORMATION:
;  APPLICANT: AMRAD Operations Pty Ltd
;  TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
;  TITLE OF INVENTION:  FAMILY OF APOPTOSIS-CONTROLLING GENES
;  FILE REFERENCE: 2096584
;  CURRENT APPLICATION NUMBER: US/09/155,327G
;  CURRENT FILING DATE:  1999-03-29
;  PRIOR APPLICATION NUMBER: PN8965
;  PRIOR FILING DATE: 1996-03-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 583
;   TYPE: DNA
;   ORGANISM: HUMAN
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(579)
US-09-155-327G-6

  Query Match             86.2%;  Score 501;  DB 4;  Length 583;
  Best Local Similarity   91.4%;  Pred. No. 3.4e-138;
  Matches  531;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;
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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||||| |||||  ||||| ||||||||||| |||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||||||| |||||||| ||||| ||||||||| ||||| ||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||| |||||||||||||| |||||||||| ||||| || ||||||
Db        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||| || ||||| ||  ||||||||
Db        301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| ||||| |||||||||||||||| || ||||  ||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||| |||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||||| |||||||||| |||||| |||||| ||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
              |||||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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RESULT 6
US-08-798-897-2
; Sequence 2, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-08-798-897-2

Query Match 85.6%; Score 497.4; DB 1; Length 579;
Best Local Similarity 91.2%; Pred. No. 3.9e-137;
Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||||| |||||  |||| ||||||||||| |||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              || |||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || ||||||||||||||||||||| ||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||| ||||| |||||||| |||||||||| |||||||||| ||||| || |||||||
Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||| || ||||| ||  ||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| ||||| |||||||||||||||| || ||||||||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              ||||| |||||||||||| |||||||||||||||||||||||||||||||||||| |||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||||| |||||||||| |||||| |||||| |||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
              |||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
```

RESULT 7
US-08-978-523-2
; Sequence 2, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/978,523
;       FILING DATE:  herewith
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/798,897
;       FILING DATE:  February 11, 1997
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Esmond, Robert W.
;       REGISTRATION NUMBER:  32,893
;       REFERENCE/DOCKET NUMBER:  1483.0140002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  579 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  both
;       TOPOLOGY:  both
;     MOLECULE TYPE:  cDNA
US-08-978-523-2

  Query Match             85.6%;  Score 497.4;  DB 2;  Length 579;
  Best Local Similarity   91.2%;  Pred. No. 3.9e-137;
  Matches  528;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  ||||||||||||| |||||  ||||  ||||||||||| |||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||||| || |||||  |||||||| || |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              || |||||||||||||||||| ||||||| |||||  |||||||| |||||  ||||||
Db        121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||||  |||||  ||||||||  || ||||||||||||||||||  ||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              |||||  |||||  ||||||||  ||||||||||  ||||||||||  |||||  ||  ||||||
Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||  ||||||||||||||||||||||  ||  |||||  ||  ||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              |||||  |||||  |||||  ||||||||||||||||  ||  ||||||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              |||||  ||||||||||  ||||||||||||||||||||||||||||||||||  ||  |||
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              ||||||||||||||  ||||||||||  ||||||  ||||||  ||||||||||||||||||||
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
              |||||||||||||||||||||||||||||||||||||||
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579

RESULT 8
US-09-010-147B-23
; Sequence 23, Application US/09010147B
; Patent No. 6653445
;   GENERAL INFORMATION:
;       APPLICANT: Ni et al.
;       TITLE OF INVENTION: Human Proteins
;       NUMBER OF SEQUENCES: 24
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Human Genome Sciences, Inc.
;           STREET: 9410 Key West Avenue
;           CITY: Rockville
;           STATE: MD
;           COUNTRY: USA
;           ZIP: 20850
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC
;                     compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/010,147B
;           FILING DATE: 12-No. 6653445-2002
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 60/034,205
;           FILING DATE: 21-JAN-1997
;           APPLICATION NUMBER: US 60/034,204
;           FILING DATE: 21-JAN-1997
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Jonathan L. Klein
;           REGISTRATION NUMBER: 41,119
;           REFERENCE/DOCKET NUMBER: PF353
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 301-309-8504
;           TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 23:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 1098 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       FEATURE:
;           NAME/KEY:  CDS
;           LOCATION:  1..1095
;       SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-010-147B-23

  Query Match             62.8%;  Score 364.8;  DB 4;  Length 1098;
  Best Local Similarity   90.3%;  Pred. No. 8.2e-98;
  Matches  390;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  ||||||||||||| |||||  ||||  ||||||||||| |||
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||||| || |||||  |||||||| || |||
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              || |||||||||||||||||| ||||||| |||||  |||||||| |||||  ||||||
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||||  |||||  ||||||||  || ||||||||||||||||||  ||||||||||||
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              |||||  |||||  ||||||||  ||||||||||  ||||||||||  |||||  ||  ||||||
Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              ||||||||||||||| |||||||||||||||||||||| || ||||| ||  |||||||||
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| ||||| ||||||||||||||||| || ||||||||||||||||||||
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGG 432
              ||||| ||||||
Db        421 AGTGGGGGCTGG 432
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RESULT 9
US-09-149-476-130
; Sequence 130, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
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; EARLIER APPLICATION NUMBER: 60/040,336
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
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; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
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; EARLIER APPLICATION NUMBER: 60/056,911
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; EARLIER APPLICATION NUMBER: 60/056,636
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; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910

; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
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; EARLIER APPLICATION NUMBER: 60/056,892
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; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
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; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 62.7%; Score 364.4; DB 3; Length 1864;
Best Local Similarity 90.0%; Pred. No. 1.4e-97;
Matches 389; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||| ||||| ||||| |||||||||||  |||
Db         11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 70

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db         71 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 130

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||||||||| ||:||||| ||||| |||||||| ||||| ||||||
Db        131 CCGCTGCACCAAGCCATGCGGGCAGCKGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 190

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || |||||||||||||||||| ||||||||||||
Db        191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 250

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||| ||||| ||||||||| |||||||||| |||||||||| ||||| || ||||||
Db        251 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 310

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||||||| || ||||| ||  ||||||||
Db        311 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 370

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| ||||| |||||||||||||||||| || ||||||||||||||||||||
Db        371 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 430

Qy        421 AGTGGCGGCTGG 432
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Db        431 AGTGGGGGCTGG 442
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RESULT 10
US-09-949-016-16799
; Sequence 16799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16799
; LENGTH: 5199
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16799

Query Match 62.7%; Score 364.2; DB 4; Length 5199;
Best Local Similarity 90.1%; Pred. No. 2.4e-97;
Matches 390; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||| ||||| ||||| |||||||||||  |||
Db       2001 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 2060

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db       2061 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 2120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              || |||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
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Db          2121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 2180
Qy           181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db          2181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 2240
Qy           241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db          2241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 2300
Qy           301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db          2301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 2360
Qy           361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db          2361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 2420
Qy           421 AGT 423
Db          2421 AGTGGGGGCTGGG 2433
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RESULT 11
US-09-949-016-177003
; Sequence 177003, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 177003
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-177003

Query Match
Best Local Similarity 61.4%; Score 357; DB 4; Length 601;
Matches 381; Conservative 90.1%; Pred. No. 1.3e-95;
1; Mismatches 41; Indels 0; Gaps 0;

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Qy             1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db           179 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 238
Qy            61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db           239 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 298
Qy           121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db           299 CCRCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 358
Qy           181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db           359 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 418
Qy           241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db           419 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 478
Qy           301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
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Db           479 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 538
Qy           361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db           539 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 598
Qy           421 AGT 423
Db           599 AGT 601
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RESULT 12
US-08-081-448-5
; Sequence 5, Application US/08081448
; Patent No. 5646008
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5646008th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,448
; FILING DATE: 19930622
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646008thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-744-0090
; TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
US-08-081-448-5

Query Match
Best Local Similarity 23.2%; Score 134.6; DB 1; Length 926;
Matches 236; Conservative 58.3%; Pred. No. 8.8e-30;
0; Mismatches 169; Indels 0; Gaps 0;

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Qy           128 ACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTG 187
Db           394 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453
Qy           188 ACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTT 247
Db           454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513
Qy           248 CCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTTG 307
Db           514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 573
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Qy        308 GGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGACAAGTCC 367
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Db        574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633

Qy        368 AGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCAGTGGCG 427
              | |||||| |   | ||||||| |    |  || |     ||||||||     |  ||||
Db        634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG 693

Qy        428 GCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGGCGTCTGC 487
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Db        694 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 753

Qy        488 GGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCG 532
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Db        754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798


RESULT 13
US-08-470-670A-6
; Sequence 6, Application US/08470670A
; Patent No. 5834309
; Patent No. 5834309 5710045
;  GENERAL INFORMATION:
;    APPLICANT:  Thompson, Craig B. B.
;    APPLICANT:  Boise, Lawrence H.
;    TITLE OF INVENTION:  VERTEBRATE APOPTOSIS GENE:
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,670A
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/081,448
;      FILING DATE:  22-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Highlander, Steven L.
;      REGISTRATION NUMBER:  37,642
;      REFERENCE/DOCKET NUMBER:  ARCD:090--1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  926 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  135..836
US-08-470-670A-6

  Query Match             23.2%;  Score 134.6;  DB 2;  Length 926;
  Best Local Similarity   58.3%;  Pred. No. 8.8e-30;
  Matches  236;  Conservative    0;  Mismatches  169;  Indels    0;  Gaps    0;

Qy        128 ACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTG 187
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Db        394 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453

Qy        188 ACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTT 247
              |||||  |  | |||||  |||  | ||||||||   ||||   |  ||   ||||    |||||
Db        454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513

Qy        248 CCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTTG 307
              | |||||  ||||  |  ||    ||||||||  ||  |||||||  ||  ||    ||| |
Db        514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 573

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Db        574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633

Qy        368 AGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCAGTGGCG 427
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Qy        428 GCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGGCGTCTGC 487
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Db        754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798


RESULT 14
US-08-481-739-1
; Sequence 1, Application US/08481739
; Patent No. 6143291
;  GENERAL INFORMATION:
;    APPLICANT:  June, Carl H. and Thompson, Craig B.
;    TITLE OF INVENTION:  METHODS FOR ENHANCING T CELL SURVIVAL
;    TITLE OF INVENTION:  BY AUGMENTING BCL-XL PROTEIN LEVELS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,739
;      FILING DATE:  07-JUNE-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/435,518
;      FILING DATE:  04-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A. (GAD)
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  RPI-034CP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  926 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  135..836
US-08-481-739-1

  Query Match             23.2%;  Score 134.6;  DB 3;  Length 926;
  Best Local Similarity   58.3%;  Pred. No. 8.8e-30;
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Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

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Db        454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513

Qy        248 CCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTTG 307
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Qy        308 GGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGACAAGTCC 367
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Qy        368 AGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCAGTGGCG 427
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Qy        488 GGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCG 532
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RESULT 15
US-09-167-921-1
; Sequence 1, Application US/09167921A
; Patent No. 6172216
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0324
; CURRENT APPLICATION NUMBER: US/09/167,921A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(836)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
US-09-167-921-1

Query Match 23.2%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 8.8e-30;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

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Db        394 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453

Qy        188 ACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTT 247
Db        454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513

Qy        248 CCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTTG 307
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Qy        308 GGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGACAAGTCC 367
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Qy        368 AGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCAGTGGCG 427
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Qy        428 GCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGGCGTCTGC 487
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Job time : 144.753 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 18:38:08 ; Search time 498.642 Seconds
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7060.905 Million cell updates/sec

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Perfect score: 581
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

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Minimum DB seq length: 0
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22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	563.4	97.0	582	9	US-09-925-674A-8	Sequence 8, Appli
	2	505.8	87.1	582	18	US-10-384-339C-37	Sequence 37, Appl
	3	505.8	87.1	583	9	US-09-925-674A-6	Sequence 6, Appli
	4	501	86.2	582	19	US-10-479-832A-4	Sequence 4, Appli
	5	364.4	62.7	1864	10	US-09-809-391-130	Sequence 130, App
	6	364.4	62.7	1864	10	US-09-882-171-130	Sequence 130, App
	7	364.4	62.7	1864	17	US-10-164-861-130	Sequence 130, App
	8	364.2	62.7	578	16	US-10-029-386-10549	Sequence 10549, A
	9	363.2	62.5	433	16	US-10-029-386-24249	Sequence 24249, A
	10	212.2	36.5	6049	15	US-10-311-455-201	Sequence 201, App
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	12	140.4	24.2	660	17	US-10-402-017-9	Sequence 9, Appli
	13	139.6	24.0	540	17	US-10-402-017-5	Sequence 5, Appli
	14	139.4	24.0	600	17	US-10-402-017-7	Sequence 7, Appli
	15	138.8	23.9	151	16	US-10-029-386-27084	Sequence 27084, A
	16	138.8	23.9	590	16	US-10-029-386-13384	Sequence 13384, A
	17	137.8	23.7	150	9	US-09-864-761-17690	Sequence 17690, A
	18	134.6	23.2	636	16	US-10-169-223-13	Sequence 13, Appl
	19	134.6	23.2	660	17	US-10-402-017-11	Sequence 11, Appl
	20	134.6	23.2	702	10	US-09-959-987-9	Sequence 9, Appli
	21	134.6	23.2	863	17	US-10-402-017-3	Sequence 3, Appli
	22	134.6	23.2	926	9	US-09-734-846-1	Sequence 1, Appli
	23	134.6	23.2	926	9	US-09-734-847A-39	Sequence 39, Appl
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	26	134.6	23.2	926	16	US-10-302-262-1	Sequence 1, Appli
	27	134.6	23.2	926	17	US-10-402-017-1	Sequence 1, Appli
	28	134.6	23.2	926	17	US-10-641-643-1430	Sequence 1430, Ap
	29	134.6	23.2	926	18	US-10-717-597-87	Sequence 87, Appl
	30	134.6	23.2	926	18	US-10-776-827-106	Sequence 106, App
	31	134.6	23.2	926	18	US-10-825-282-47	Sequence 47, Appl
	32	134.6	23.2	926	19	US-10-479-832A-3	Sequence 3, Appli
	33	134.6	23.2	1236	18	US-10-792-517-1	Sequence 1, Appli
	34	130.6	22.5	1455	18	US-10-792-517-7	Sequence 7, Appli
c	35	126.8	21.8	600	9	US-09-864-761-7360	Sequence 7360, Ap
	36	126.6	21.8	720	17	US-10-148-953A-8	Sequence 8, Appli
	37	126.4	21.8	1466	18	US-10-283-975A-394	Sequence 394, App
	38	125.8	21.7	492	10	US-09-918-995-33305	Sequence 33305, A
c	39	125.8	21.7	555	9	US-09-864-761-24081	Sequence 24081, A
c	40	125.8	21.7	564	16	US-10-029-386-20790	Sequence 20790, A
	41	125	21.5	717	16	US-10-053-645A-20	Sequence 20, Appl
	42	125	21.5	720	17	US-10-148-953A-6	Sequence 6, Appli
	43	125	21.5	720	17	US-10-148-953A-7	Sequence 7, Appli
	44	125	21.5	720	17	US-10-297-321-1	Sequence 1, Appli
	45	125	21.5	720	18	US-10-770-668-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-925-674A-8
; Sequence 8, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(579)
US-09-925-674A-8

Query Match 97.0%; Score 563.4; DB 9; Length 582;
Best Local Similarity 98.1%; Pred. No. 2.9e-160;
Matches 570; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy       121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
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Qy       181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db       181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy       241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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Qy       301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
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Qy       361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
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Db       421 AGTGGCGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

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RESULT 2
US-10-384-339C-37
; Sequence 37, Application US/10384339C
; Publication No. US20040175703A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Roland
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE
; FILE REFERENCE: 20200/2002
; CURRENT APPLICATION NUMBER: US/10/384,339C
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: DE 10155280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 10158411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 10160151.4
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: bcl-w
; PATENT DOCUMENT NUMBER: U59747
US-10-384-339C-37

Query Match 87.1%; Score 505.8; DB 18; Length 582;
Best Local Similarity 91.9%; Pred. No. 7.8e-143;
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Qy       181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db       541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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RESULT 3
US-09-925-674A-6
; Sequence 6, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 583
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(579)
US-09-925-674A-6

Query Match 87.1%; Score 505.8; DB 9; Length 583;
Best Local Similarity 91.9%; Pred. No. 7.8e-143;
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Qy         1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db         1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db        241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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RESULT 4
US-10-479-832A-4
; Sequence 4, Application US/10479832A
; Publication No. US20050064407A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson Research Pty Ltd
; TITLE OF INVENTION: bcl-2 DNAzymes
; FILE REFERENCE: WJP13107942
; CURRENT APPLICATION NUMBER: US/10/479,832A
; CURRENT FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-479-832A-4

Query Match 86.2%; Score 501; DB 19; Length 582;
Best Local Similarity 91.4%; Pred. No. 2.2e-141;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db         61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db        121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db        241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db        301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db        361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCAGCTGGCTGACTGGATCCACAGC 420

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
Db        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
Db        481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
Db        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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RESULT 5
US-09-809-391-130
; Sequence 130, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1648)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-809-391-130

Query Match 62.7%; Score 364.4; DB 10; Length 1864;
Best Local Similarity 90.0%; Pred. No. 5.4e-100;
Matches 389; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db         11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 70

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db         71 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 130

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db        131 CCGCTGCACCAAGCCATGCGGGCAGCKGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 190

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 250

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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Db        251 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 310

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              ||||||||||||||| |||||||||||||||||||||| || ||||| ||  ||||||||
Db        311 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 370

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| ||||| |||||||||||||||| || ||||||||||||||||||||
Db        371 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 430

Qy        421 AGTGGCGGCTGG 432
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Db        431 AGTGGGGGCTGG 442
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RESULT 6
US-09-882-171-130
; Sequence 130, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
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; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/047,617
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; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
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; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/043,315
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/056,886
; PRIOR FILING DATE: 1997-08-22
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; PRIOR APPLICATION NUMBER: 60/057,761
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; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
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; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
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; PRIOR APPLICATION NUMBER: 60/056,876
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; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match 62.7%; Score 364.4; DB 10; Length 1864;
Best Local Similarity 90.0%; Pred. No. 5.4e-100;
Matches 389; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||||| ||||| ||||| |||||||||||| |||
Db         11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 70

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db         71 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 130

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||||||| ||:||||| ||||| |||||||| ||||| ||||||
Db        131 CCGCTGCACCAAGCCATGCGGGCAGCKGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 190

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || |||||||||||||||||||| ||||||||||||
Db        191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 250

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||| ||||| |||||||| |||||||||| ||||| || ||||||
Db        251 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 310

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||||||| || ||||| ||  ||||||||
Db        311 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 370

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| |||||| |||||||||||||||| || ||||||||||||||||||||
Db        371 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 430

Qy        421 AGTGGCGGCTGG 432
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Db        431 AGTGGGGGCTGG 442
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RESULT 7
US-10-164-861-130
; Sequence 130, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1648)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-164-861-130

Query Match 62.7%; Score 364.4; DB 17; Length 1864;
Best Local Similarity 90.0%; Pred. No. 5.4e-100;
Matches 389; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

```
Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||||| ||||| ||||| |||||||||||| |||
Db         11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 70

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db         71 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 130
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Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db        131 CCGCTGCACCAAGCCATGCGGGCAGCKGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 190

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 250

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db        251 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 310

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db        311 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 370

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db        371 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 430

Qy        421 AGTGGCGGCTGG 432
Db        431 AGTGGGGGCTGG 442
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RESULT 8
US-10-029-386-10549
; Sequence 10549, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10549
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 0.00e+00
; OTHER INFORMATION: NT HIT: gi14751151, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALUE 2.00e-72
US-10-029-386-10549

Query Match 62.7%; Score 364.2; DB 16; Length 578;
Best Local Similarity 90.1%; Pred. No. 5.4e-100;
Matches 390; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db        105 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 164

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db        165 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 224

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db        225 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 284

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        285 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 344

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db        345 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 404

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db        405 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 464

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db        465 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCAGCTGGCTGACTGGATCCACAGC 524

Qy        421 AGTGGCGGCTGGG 433
Db        525 AGTGGGGGCTGGG 537
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RESULT 9
US-10-029-386-24249
; Sequence 24249, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24249
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALUE 2.00e-72
; OTHER INFORMATION: NT HIT: gi14751151, EVALUE 0.00e+00
US-10-029-386-24249

Query Match 62.5%; Score 363.2; DB 16; Length 433;
Best Local Similarity 90.0%; Pred. No. 1e-99;
Matches 389; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db          2 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 61

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db         62 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 121

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db        122 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 181

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        182 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 241
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Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db        242 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 301

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db        302 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 361

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db        362 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCAGCTGGCTGACTGGATCCACAGC 421

Qy        421 AGTGGCGGCTGG 432
Db        422 AGTGGGGGCTGG 433

RESULT 10
US-10-311-455-201
; Sequence 201, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 201
;   LENGTH: 6049
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-201

  Query Match              36.5%;  Score 212.2;  DB 15;  Length 6049;
  Best Local Similarity    68.1%;  Pred. No. 7e-54;
  Matches  295;  Conservative    0;  Mismatches  138;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db       5001 ATGGCGATTTTAGTTTCGGTTTTAGATATACGGGTTTTGGTGGTAGATTTTGTAGGTTAT 5060

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db       5061 AAGTTGAGGTAGAAGGGTTATGTTTGTGGAGTTGGTTTCGGGGAGGGTTTAGTAGTTGAT 5120

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db       5121 TCGTTGTATTAAGTTATGCGGGTAGTTGGAGATGAGTTCGAGATTCGTTTTCGGCGTATT 5180

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db       5181 TTTTTTGATTTGGCGGTTTAGTTGTATGTGATTTTAGGTTTAGTTTAATAACGTTTTATT 5240

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db       5241 TAGGTTTTCGATGAATTTTTTTAAGGGGGTTTTAATTGGGGTCGTTTTGTAGTTTTTTTT 5300

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db       5301 GTTTTTGGGGTTGTATTGTGTGTTGAGAGTGTTAATAAGGAGATGGAATTATTGGTGGGA 5360

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db       5361 TAAGTGTAGGAGTGGATGGTGGTTTATTTGGAGACGTAGTTGGTTGATTGGATTTATAGT 5420

Qy        421 AGTGGCGGCTGGG 433
Db       5421 AGTGGGGGTTGGG 5433

RESULT 11
US-10-311-455-202/c
; Sequence 202, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determi
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 202
;   LENGTH: 6049
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-202

  Query Match              32.9%;  Score 191;  DB 15;  Length 6049;
  Best Local Similarity    65.7%;  Pred. No. 1.8e-47;
  Matches  278;  Conservative    0;  Mismatches  145;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db       1049 ATAACGACCCCAACCTCGACCCCAAACACACGAACTCTAATAACAAACTTTATAAATTAT 990

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
Db        989 AAACTAAAACAAAAAAATTATATCTATAAAACTAACCCCGAAAAAAACCCAACAACTAAC 930

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db        929 CCGCTACACCAAACCATACGAACAACTAAAAATAAATTCGAAACCCGCTTCCGACGCACC 870

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db        869 TTCTCTAATCTAACGACTCAACTACATATAACCCCAAACTCAACCCAACAACGCTTCACC 810

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db        809 CAAATCTCCGATAAACTTTTTCAAAAAAACCCCAACTAAAACCGCCTTATAACCTTCTTT 750

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db        749 ATCTTTAAAACTACACTATATACTAAAAATATCAACAAAAAAATAAAACCACTAATAAAA 690

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db        689 CAAATACAAAAATAAATAATAACCTACCTAAAAACGCAACTAACTAACTAAATCCACAAC 630

Qy        421 AGT 423
Db        629 AAT 627
```

```
RESULT 12
US-10-402-017-9
; Sequence 9, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
;  APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
;  TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
;  TITLE OF INVENTION:  such cells
;  FILE REFERENCE: Case 1/1314
;  CURRENT APPLICATION NUMBER: US/10/402,017
;  CURRENT FILING DATE:  2003-03-28
;  PRIOR APPLICATION NUMBER: US 60/369,307
;  PRIOR APPLICATION NUMBER: April 2, 2002
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 660
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Deletion mutant of SEQ ID NO:3 (del66-83)
US-10-402-017-9

  Query Match             24.2%;  Score 140.4;  DB 17;  Length 660;
  Best Local Similarity   57.5%;  Pred. No. 2.8e-32;
  Matches  252;  Conservative    0;  Mismatches  186;  Indels    0;  Gaps    0;

Qy         95 GGCCTGGGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGAGACG 154
Db        185 GCCCCGCGGTAGCGGCCGCAGCAGCAGCCGTAAAGCAAGCGCTGAGAGAGGCCGGCGATG 244

Qy        155 AGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCAGCTACACGTGACCC 214
Db        245 AGTTTGAGCTGCGGTACCGGCGGGCGTTCAGTGATCTAACATCCCAGCTTCATATAACCC 304

Qy        215 CAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTA 274
Db        305 CAGGGACTGCATATCAAAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAA 364

Qy        275 ACTGGGGCCGTCTTGTGGCATTCTTTGTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCA 334
Db        365 ACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCGGTGGAGCCCTCTGTGTGGAAAGCGTAG 424

Qy        335 ACAAAGAAATGGAGCCTTTGGTGGGACAAGTCCAGGATTGGATCGTGGCCTACCTGGAGA 394
Db        425 ACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAAGTTGGATGGCCACCTACCTGAATG 484

Qy        395 CACGTCTGGCTGACTGGATCCACAGCAGTGGCGGCTGGGCGGACTTCACAGCTCTATACG 454
Db        485 ACCACCTAGAGCCTTGGATCCAGGACAACGGCGGCTGGGACACTTTCGTGGAACTCTACG 544

Qy        455 GGGACGGGGCCCTGGAGGACGCACGGCGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCA 514
Db        545 GAAACAATGCAGCAGCTGAGAGCCGGAAAGGCCAGGAGCGCTTCAACCGCTGGTTCCTGA 604

Qy        515 CAGTGGTGACGGGGGCCG 532
Db        605 CGGGCATGACTGTGGCTG 622

RESULT 13
US-10-402-017-5
; Sequence 5, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
;  APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
;  TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
;  TITLE OF INVENTION:  such cells
;  FILE REFERENCE: Case 1/1314
;  CURRENT APPLICATION NUMBER: US/10/402,017
;  CURRENT FILING DATE:  2003-03-28
;  PRIOR APPLICATION NUMBER: US 60/369,307
;  PRIOR APPLICATION NUMBER: April 2, 2002
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 540
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Deletion mutant of SEQ ID NO:3 (del26-83)
US-10-402-017-5

  Query Match             24.0%;  Score 139.6;  DB 17;  Length 540;
  Best Local Similarity   56.7%;  Pred. No. 4.8e-32;
  Matches  287;  Conservative    0;  Mismatches  204;  Indels   15;  Gaps    1;

Qy         27 CACACGCGCTCTAGTGGCTGACTTTGTAGGCTATAGGCTGAGGCAGAAGGGTTATGTCTG 86
Db         12 CAACCGGGAGCTAGTGGTTGACTTTCTCTCCTACAAGCTCTCCCAGAAAGGATACAGCTG 71

Qy         87 TGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGC 146
Db         72 GAGTGCGG---------------CCGCAGCAGCAGCCGTAAAGCAAGCGCTGAGAGAGGC 116

Qy        147 TGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCAGCTACA 206
Db        117 CGGCGATGAGTTTGAGCTGCGGTACCGGCGGGCGTTCAGTGATCTAACATCCCAGCTTCA 176

Qy        207 CGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCGACGAACTTTTCCAAGG 266
Db        177 TATAACCCCAGGGACTGCATATCAAAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGA 236

Qy        267 GGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTTGGGGCTGCCCTGTGTGCTGA 326
Db        237 TGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCGGTGGAGCCCTCTGTGTGGA 296

Qy        327 GAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGACAAGTCCAGGATTGGATCGTGGCCTA 386
Db        297 AAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAAGTTGGATGGCCACCTA 356

Qy        387 CCTGGAGACACGTCTGGCTGACTGGATCCACAGCAGTGGCGGCTGGGCGGACTTCACAGC 446
Db        357 CCTGAATGACCACCTAGAGCCTTGGATCCAGGACAACGGCGGCTGGGACACTTTCGTGGA 416

Qy        447 TCTATACGGGGACGGGGCCCTGGAGGACGCACGGCGTCTGCGGGAGGGCAACTGGGCATG 506
Db        417 ACTCTACGGAAACAATGCAGCAGCTGAGAGCCGGAAAGGCCAGGAGCGCTTCAACCGCTG 476

Qy        507 AGTGAGCACAGTGGTGACGGGGGCCG 532
Db        477 GTTCCTGACGGGCATGACTGTGGCTG 502

RESULT 14
US-10-402-017-7
; Sequence 7, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
;  APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
;  TITLE OF INVENTION: Host cells having improved survival properties and methods to gene
;  TITLE OF INVENTION:  such cells
;  FILE REFERENCE: Case 1/1314
;  CURRENT APPLICATION NUMBER: US/10/402,017
;  CURRENT FILING DATE:  2003-03-28
;  PRIOR APPLICATION NUMBER: US 60/369,307
;  PRIOR APPLICATION NUMBER: April 2, 2002
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 600
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
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;   OTHER INFORMATION: Deletion mutant of SEQ ID NO:3 (del46-83)
US-10-402-017-7

  Query Match             24.0%;  Score 139.4;  DB 17;  Length 600;
  Best Local Similarity   57.1%;  Pred. No. 5.6e-32;
  Matches  254;  Conservative    0;  Mismatches  191;  Indels    0;  Gaps    0;

Qy         88 GGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCT 147
              ||| |||   | | |   |  | || || |  |  |  | |||||  || | |  ||
Db        118 GGAACTGAATCAGAGAGGGCGGCCGCAGCAGCAGCCGTAAAGCAAGCGCTGAGAGAGGCC 177

Qy        148 GGAGACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCAGCTACAC 207
              || || |||||||||   || | ||| ||  | |||  ||| ||  |  | |||||  ||
Db        178 GGCGATGAGTTTGAGCTGCGGTACCGGCGGGCGTTCAGTGATCTAACATCCCAGCTTCAT 237

Qy        208 GTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCGACGAACTTTTCCAAGGG 267
              | ||||||||  | ||  | ||| ||||    |||||     | |||||  ||||  |
Db        238 ATAACCCCAGGGACTGCATATCAAAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGAT 297

Qy        268 GGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTTGGGGCTGCCCTGTGTGCTGAG 327
              ||    |||||||| ||  |||||||| || ||   ||| || |  |||||  ||||  ||
Db        298 GGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCGGTGGAGCCCTCTGTGTGGAA 357

Qy        328 AGTGTCAACAAAGAAATGGAGCCTTTGGTGGGACAAGTCCAGGATTGGATCGTGGCCTAC 387
              || ||  |||| || ||| ||   |||||| | |   ||     ||||||  |  |||||
Db        358 AGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAAGTTGGATGGCCACCTAC 417

Qy        388 CTGGAGACACGTCTGGCTGACTGGATCCACAGCAGTGGCGGCTGGGCGGACTTCACAGCT 447
              |||  |    |  || |     |||||||    ||  ||||||||||      |||   |
Db        418 CTGAATGACCACCTAGAGCCTTGGATCCAGGACAACGGCGGCTGGGACACTTTCGTGGAA 477

Qy        448 CTATACGGGGACGGGGCCCTGGAGGACGCACGGCGTCTGCGGGAGGGCAACTGGGCATGA 507
              || |||||  ||   ||   |  ||   |||      | |||| ||  |       ||
Db        478 CTCTACGGAAACAATGCAGCAGCTGAGAGCCGGAAAGGCCAGGAGCGCTTCAACCGCTGG 537

Qy        508 GTGAGCACAGTGGTGACGGGGGCCG 532
              |    || |   |||| | ||| |
Db        538 TTCCTGACGGGCATGACTGTGGCTG 562


RESULT 15
US-10-029-386-27084
; Sequence 27084, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27084
;   LENGTH: 151
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR14.3
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
;   OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 5.00e-70
;   OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11
;   OTHER INFORMATION: NT HIT: gi14574571, EVALUE 9.00e-80
US-10-029-386-27084

  Query Match             23.9%;  Score 138.8;  DB 16;  Length 151;
  Best Local Similarity   95.3%;  Pred. No. 7.1e-32;
  Matches  143;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        432 GGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGGCGTCTGCGGGA 491
              |||||| |||||||||||||||||||||||||||||||| || ||||||||||||||
Db          1 GGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGA 60

Qy        492 GGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTGGGGGCCCTGGT 551
              ||| |||||||||| |||||| |||||| ||||||||||||||||||||||||||||||
Db         61 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGT 120

Qy        552 AACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
              ||||||||||||||||||||||||||||||
Db        121 AACTGTAGGGGCCTTTTTTGCTAGCAAGTG 150


Search completed: April 10, 2005, 22:38:34
Job time : 500.642 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 14:47:25 ; Search time 2831.63 Seconds
(without alignments)
7810.120 Million cell updates/sec

Title: US-09-925-674B-8
Perfect score: 581
Sequence: 1 atgccgacccccagcctcaac.....gccttttttgctagcaagtg 581

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	560.2	96.4	582	9	AY421022	AY421022 Mus muscu
2	560.2	96.4	1949	3	AK015644	AK015644 Mus muscu
3	560.2	96.4	3487	3	AK004680	AK004680 Mus muscu
4	558.6	96.1	969	6	BY715200	BY715200 BY715200
5	503.6	86.7	967	5	BU503850	BU503850 AGENCOURT
6	501	86.2	582	9	AY421020	AY421020 Homo sapi
c 7	501	86.2	727	6	CD617893	CD617893 56057475J
c 8	499.4	86.0	629	6	CD617891	CD617891 56057367J
9	477.6	82.2	804	1	AL157542	AL157542 DKFZp761D
10	477	82.1	1030	2	BE793530	BE793530 601590016
11	471.2	81.1	713	5	BP753931	BP753931 BP753931
12	456.6	78.6	757	7	CK359685	CK359685 AGENCOURT
13	456	78.5	643	7	CN281020	CN281020 170005318
14	447.8	77.1	662	6	CD617892	CD617892 56057475H
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16	429	73.8	815	2	BF785386	BF785386 602111728
17	421.8	72.6	854	3	AK013244	AK013244 Mus muscu
18	413	71.1	697	4	BI770566	BI770566 603060362
19	409	70.4	792	4	BG298789	BG298789 602396527
20	407.4	70.1	623	6	CB578463	CB578463 AMGNNUC:N
21	403.6	69.5	540	2	AW258810	AW258810 um74a02.y
22	387.2	66.6	516	7	CN281015	CN281015 170005321
23	382.2	65.8	626	6	CA391923	CA391923 cs20c09.y
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25	364.6	62.8	752	7	CO401477	CO401477 AGENCOURT
26	364	62.7	583	5	BP355256	BP355256 BP355256
27	362.2	62.3	583	5	BP249141	BP249141 BP249141
28	362.2	62.3	584	5	BP311709	BP311709 BP311709
29	359.4	61.9	583	5	BP202031	BP202031 BP202031
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31	353.6	60.9	440	6	CB749817	CB749817 AMGNNUC:M
32	348.4	60.0	559	6	BY704881	BY704881 BY704881
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35	323.8	55.7	645	6	BY740551	BY740551 BY740551
36	321.8	55.4	362	1	AA596919	AA596919 vo21f08.r
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44	294	50.6	582	5	BP216712	BP216712 BP216712
45	283.8	48.8	1053	5	BU931540	BU931540 AGENCOURT

ALIGNMENTS

RESULT 1
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LOCUS AY421022 582 bp DNA linear GSS 17-DEC-2003
DEFINITION Mus musculus BCL2L2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY421022
VERSION AY421022.1 GI:39776979
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 582)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 582)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
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gene <1. .>582
/gene="BCL2L2"
/locus_tag="HCM7418"
ORIGIN

Query Match 96.4%; Score 560.2; DB 9; Length 582;
Best Local Similarity 97.8%; Pred. No. 3.2e-134;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60

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Db          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

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Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
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RESULT 2
AK015644

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DEFINITION  Mus musculus adult male testis cDNA, RIKEN full-length enriched
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            sequence.
ACCESSION   AK015644
VERSION     AK015644.1  GI:12854052
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1949)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
            Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
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            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
            Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
            Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.jp/) for further
            details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCC 3']. cDNA was cleaved
            with BamHI and XhoI. cDNA of size comprised longer than 7 kb was
            selected before cloning. Vector: a modified pBluescript KS(+) after
            bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
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ORIGIN

Query Match 96.4%; Score 560.2; DB 3; Length 1949;
Best Local Similarity 97.8%; Pred. No. 3.9e-134;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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Db        132 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 191

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
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Db        192 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 251

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
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Db        252 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 311

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        312 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 371

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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Db        372 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 431

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
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Db        432 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 491

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
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Db        492 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 551

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
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RESULT 3
AK004680
LOCUS AK004680 3487 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200009L24 product:Bcl2-like 2, full insert sequence.
ACCESSION AK004680
VERSION AK004680.1 GI:12836027
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3487)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGAGAGAGAAGGATCCAAGAGCTCAATTAATTTAATTAAACCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

FEATURES Location/Qualifiers
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/sex="male"

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ORIGIN

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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Db        449 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 508

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
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Db        569 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 628

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
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Db        629 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 688

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
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Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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RESULT 4
BY715200
LOCUS       BY715200                969 bp    mRNA    linear   EST 17-DEC-2002
DEFINITION  BY715200 RIKEN full-length enriched, adult male testis Mus musculus
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ACCESSION   BY715200
VERSION     BY715200.1  GI:27128317
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 969)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
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            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
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            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
            Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
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            Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
            Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES                Location/Qualifiers
     source             1. .969
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/lab_host="SOLR"
/clone_lib="RIKEN full-length enriched, adult male testis"
/note="Site_1: XhoI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAGCGGCCGCAATTAATTCTCGAGTTAATTAAATTAATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. "

ORIGIN

Query Match 96.1%; Score 558.6; DB 6; Length 969;
Best Local Similarity 97.6%; Pred. No. 9.1e-134;
Matches 567; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Db        132 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 191

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
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Db        192 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 251

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
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Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        312 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 371

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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Db        372 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 431

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
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Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
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Db        552 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 611

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Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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Db        672 GGGGCTCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 712
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RESULT 5
BU503850

LOCUS BU503850 967 bp mRNA linear EST 12-SEP-2002
DEFINITION AGENCOURT_10030867 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6491566 5', mRNA sequence.
ACCESSION BU503850
VERSION BU503850.1 GI:22810083
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 967)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14043 row: c column: 23
High quality sequence stop: 524.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 86.7%; Score 503.6; DB 5; Length 967;
Best Local Similarity 96.8%; Pred. No. 1.6e-119;
Matches 567; Conservative 0; Mismatches 14; Indels 5; Gaps 5;

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Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
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Db        370 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 429

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Qy        361 CAAGTCCAGGATTGGATCGTGGCCTA-CCTGGAGACACGTCTGGCTGACTGGATCCACAG 419
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Qy        420 CAGT-GGCGGCTGGGCGGACTTCACAGCTCTATACGGGGAC-GGGGCCCTGGAGGACGCA 477
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RESULT 6
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LOCUS AY421020 582 bp DNA linear GSS 17-DEC-2003
DEFINITION Homo sapiens BCL2L2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY421020
VERSION AY421020.1 GI:39776977
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 582)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.
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ORIGIN

Query Match 86.2%; Score 501; DB 9; Length 582;
Best Local Similarity 91.4%; Pred. No. 7e-119;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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RESULT 7
CD617893/c
LOCUS CD617893 727 bp mRNA linear EST 12-JAN-2004
DEFINITION 56057475J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD617893
VERSION CD617893.1 GI:40266158
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 727)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES Location/Qualifiers
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/note="Vector: pDrive Cloning Vector"
ORIGIN

Query Match 86.2%; Score 501; DB 6; Length 727;
Best Local Similarity 91.4%; Pred. No. 7.2e-119;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
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Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        488 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 429

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        428 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 369

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Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Db        308 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 249

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Db        248 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 189

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480

Db        188 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 129

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540

Db        128 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 69

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581

Db         68 GGGGCACTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 28
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RESULT 8
CD617891/c
LOCUS CD617891 629 bp mRNA linear EST 12-JAN-2004
DEFINITION 56057367J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD617891
VERSION CD617891.1 GI:40266156
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 629)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES Location/Qualifiers
source 1. .629
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
ORIGIN

Query Match 86.0%; Score 499.4; DB 6; Length 629;
Best Local Similarity 91.2%; Pred. No. 1.8e-118;
Matches 530; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Db        607 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 548

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120

Db        547 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 488

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180

Db        487 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 428
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```
Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Db        427 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 368

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300

Db        367 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 308

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Db        307 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 248

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Db        247 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 188

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480

Db        187 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 128

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540

Db        127 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 68

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581

Db         67 GGGGCCTCGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 27
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RESULT 9
AL157542
LOCUS AL157542 804 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp761D0816_r1 761 (synonym: hamy2) Homo sapiens cDNA clone
DKFZp761D0816 5', mRNA sequence.
ACCESSION AL157542
VERSION AL157542.1 GI:7057943
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 804)
AUTHORS Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.
TITLE EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp761D0816) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES Location/Qualifiers
source 1. .804
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp761D0816"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="761 (synonym: hamy2)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
ORIGIN

Query Match 82.2%; Score 477.6; DB 1; Length 804;

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  Best Local Similarity   91.0%;  Pred. No. 8.5e-113;
  Matches  529;  Conservative    0;  Mismatches   50;  Indels    2;  Gaps    2;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||||| ||||| ||||| |||||||||||| |||
Db        134 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 193

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db        194 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 253

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        254 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 313

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || |||||||||||||||||||| ||||||||||||
Db        314 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 373

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||| ||||| |||||||| |||||||||| |||||||||| ||||| || |||||||
Db        374 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 433

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||| |||||||| ||||||||||||||| || ||||| ||  ||||||||
Db        434 GTCTTTGGGGCTGCACTGTGTGCNGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 493

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| ||||| |||||||||||||||| || ||||||||||||||||||||||
Db        494 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 553

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              ||||| |||||||||||| |||||||||||||||||||| |||||||||||||| || |||
Db        554 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGAC-GGGCCCTGGAGGAGGCGCGG 612

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||||| |||||||||| |||||| |||||| ||||||||||||||||||||
Db        613 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACT- 671

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
              |||||||||||||||||||||||||||||||||||||||||
Db        672 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 712
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RESULT 10
BE793530
LOCUS BE793530 1030 bp mRNA linear EST 20-SEP-2000
DEFINITION 601590016F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944307 5', mRNA sequence.
ACCESSION BE793530
VERSION BE793530.1 GI:10214832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1030)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM800 row: p column: 04
High quality sequence start: 5
High quality sequence stop: 709.
FEATURES Location/Qualifiers
source 1. .1030
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3944307"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

```
  Query Match             82.1%;  Score 477;  DB 2;  Length 1030;
  Best Local Similarity   88.8%;  Pred. No. 1.3e-112;
  Matches  516;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||  |||||||||||||| ||||| ||||| |||||||||||| |||
Db        144 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 203

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db        204 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 263

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              || |||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db        264 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 323

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              |||||||| ||||| |||||||| || |||||||||||||||||||| ||||||||||||
Db        324 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 383

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              ||||| ||||| |||||||| |||||||||| |||||||||| ||||| || |||||||
Db        384 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 443

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||| |||||||||||||||||||||||| || ||||| ||  ||||||||
Db        444 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 503

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| ||||| ||||| |||||||||||||||| || ||||||||||||||||||||||
Db        504 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 563

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              ||||| |||||||||||| |||||||||||||||||||||||||||||||||||| || |||
Db        564 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 623

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540
              |||||||||||  ||  |||||||| |||||| |||||| ||||||||| ||||||||||
Db        624 CGTCTGCGGGGAGGGGACTGGGCATCAGTGAGGACAGTGCTGACGGGGGGCGTGGCACTG 683

Qy        541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
              ||||  |||||  |      ||| | ||||||||||||||||
Db        684 GGGGGCCTGGGTAACTGTAGGGGCCTTTTTGCTAGCAAGTG 724
```

RESULT 11
BP753931
LOCUS BP753931 713 bp mRNA linear EST 08-JUL-2004
DEFINITION BP753931 mouse (C57BL/6) pancreatic islet library with recombination-based method Mus musculus cDNA clone mia06063 5', mRNA sequence.
ACCESSION BP753931
VERSION BP753931.1 GI:50073821
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

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  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 713)
  AUTHORS   Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
            Takeda,J., Ohara,O. and Seino,S.
  TITLE     Construction of a multi-functional cDNA library specific for mouse
            pancreatic islets and its application to microarray
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Susumu Seino
            Division of Cellular and Molecular Medicine
            Kobe University Graduate School of Medicine
            7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
            Tel: 81-78-382-5360
            Fax: 81-78-382-5370
            Email: seino@med.kobe-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .713
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="mia06063"
                     /sex="male"
                     /tissue_type="pancratic islet"
                     /dev_stage="adult"
                     /clone_lib="mouse (C57BL/6) pancreatic islet library with
                     recombination-based method"
ORIGIN

  Query Match             81.1%;  Score 471.2;  DB 5;  Length 713;
  Best Local Similarity   95.3%;  Pred. No. 3.8e-111;
  Matches  551;  Conservative    0;  Mismatches   18;  Indels    9;  Gaps    6;

Qy          2 TGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTATA 61
              || |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         34 TGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTATA 93

Qy         62 GGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGACC 121
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         94 AGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGACC 153

Qy        122 CGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCT 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 CGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCT 213

Qy        182 TCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCC 273

Qy        242 AGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTG 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTG 333

Qy        302 TCTTTGGGGCTG-CCCTGTGTGCTGAGAGTGTCAAC-AAAGAAATGGAGCCTTTGG--TG 357
              |||||||||||| |||||||||||||||||||||| |||||||||||||||||||    |
Db        334 TCTTTGGGGCTGCCCCTGTGTGCTGAGAGTGTCAACAAAAGAAATGGAGCCTTTGGGTGG 393

Qy        358 GGACAAGTCCAGGATTGG--ATCGTGGCCTACCT-GGAGACACGTCTGGCTGACTGGATC 414
              |||||||| |||||||||     |||||||||||| |||||||||||||||||||||||||
Db        394 GGACAAGTGCAGGATTGGGATGGGTGGCCTACCTGGGAGACACGTCTGGCTGACTGGATC 453

Qy        415 CACAGCAGTGGCGG--CTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGG 472
              |||||||||||  ||    |||||||| |||||||||||||||||||||||||||||||||
Db        454 CACAGCAGTGGGGGGCTGGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGG 513

Qy        473 ACGCACGGCGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCG 532
              | |||||||||||||||||| |||||||||| |||||| |||||| ||||||||||||
Db        514 AGGCACGGCGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCG 573

Qy        533 TGGCACTGGGGGCCCTGGTAACTGTAGGGGCCTTTTTT 570
              ||||||||||||||||||||||||||||||||||||||
Db        574 TGGCACTGGGGGCCCTGGTAACTGTAGGGGCCTTTTTT 611
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```
RESULT 12
CK359685
LOCUS       CK359685                757 bp    mRNA    linear   EST 23-DEC-2003
DEFINITION  AGENCOURT_17156314 NIH_MGC_233 Rattus norvegicus cDNA clone
            IMAGE:7105621 5', mRNA sequence.
ACCESSION   CK359685
VERSION     CK359685.1  GI:40325617
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 757)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Howard Jacobs
             cDNA Library Preparation: Express Genomics
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14965  row: a  column: 11
            High quality sequence start: 20
            High quality sequence stop: 702.
FEATURES             Location/Qualifiers
     source          1. .757
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="IMAGE:7105621"
                     /tissue_type="heart, pooled"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_233"
                     /note="Organ: heart; Vector: pExpress-1; Site_1: EcoRV;
                     Site_2: NotI; RNA obtained from pooled heart tissue from a
                     mix of male and female animals at 8 wk old. Tissues were
                     snap-frozen and kept at -80C for two days before RNA
                     extraction and purification (Tri-reagent method). cDNA was
                     primed using oligo-dT primer:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
                     resulted in an average insert size of 2 kb. This primary
                     library is not normalized (normalized primary library is
                     NIH_MGC_234) and was constructed by Express Genomics
                     (Frederick, MD). Note: this is a NIH_MGC library."
ORIGIN

  Query Match             78.6%;  Score 456.6;  DB 7;  Length 757;
  Best Local Similarity   95.9%;  Pred. No. 2.3e-107;
  Matches  490;  Conservative    0;  Mismatches   19;  Indels    2;  Gaps    2;

Qy          1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
              ||| |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        233 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 292

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | ||||||||||||||||||||||||||||||| |||||||||||||||| ||||||
Db        293 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 352

Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
              |||||||||||||||||||||| |||||||||||||||||||||||| ||||| ||||||
Db        353 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 412
```

```
Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 472

Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        473 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 532

Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        533 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 592

Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
              ||||| |||||||||||| ||| ||||||||||||||| ||||||||||||||||||||
Db        593 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 652

Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
              ||||| |||||||||||| ||||||||||||||||||||||||||||||||| ||||||
Db        653 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGA-GCACGG 711

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGA 511
              ||||||||||||||  ||||||||| |||||
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RESULT 13
CN281020
LOCUS       CN281020                643 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000531876837 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN281020
VERSION     CN281020.1  GI:47297434
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 643   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .643
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                     conditions."
ORIGIN

  Query Match             78.5%;  Score 456;  DB 7;  Length 643;
  Best Local Similarity   90.7%;  Pred. No. 3.2e-107;
  Matches  486;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

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Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
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Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
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Db        228 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 287

Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Db        288 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 347

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Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
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Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
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Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
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Db        528 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 587

Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGC 536
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RESULT 14
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LOCUS       CD617892                662 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  56057475H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD617892
VERSION     CD617892.1  GI:40266157
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 662)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .662
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ORIGIN

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  Best Local Similarity   90.2%;  Pred. No. 4.3e-105;
  Matches  490;  Conservative    0;  Mismatches   52;  Indels    1;  Gaps    1;

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Db        120 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 179

Qy         61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
              | |||||||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
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Db        180 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 239
Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
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Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db        360 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 419
Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db        420 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 479
Qy        361 CAAGTCCAGGATTGGA-TCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAG 419
Db        480 CAAGTGCAGGAGTGGATTGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAG 539
Qy        420 CAGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACG 479
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Qy        480 GCGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACT 539
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Db        660 GGG 662
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RESULT 15
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DEFINITION 56057367H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD617890
VERSION CD617890.1 GI:40266155
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 627)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/note="Vector: pDrive Cloning Vector"
ORIGIN

Query Match 74.5%; Score 432.8; DB 6; Length 627;
Best Local Similarity 90.7%; Pred. No. 3.3e-101;
Matches 461; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Qy        121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
Db        240 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 299
Qy        181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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Qy        241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
Db        360 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 419
Qy        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
Db        420 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 479
Qy        361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
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Qy        421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
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Qy        481 CGTCTGCGGGAGGGCAACTGGGCATGAG 508
Db        600 CGTCTGCGGGAGGGGAACTGGGCATCAG 627
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 10, 2005, 22:21:58 ; Search time 19.5 Seconds
(without alignments)
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Title: US-09-925-674B-9
Perfect score: 1009
Sequence: 1 MATPASTPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1009	100.0	193	4	US-09-155-327G-9	Sequence 9, Appli
2	1005	99.6	193	1	US-08-798-897-3	Sequence 3, Appli
3	1005	99.6	193	2	US-08-978-523-3	Sequence 3, Appli
4	1000	99.1	192	1	US-08-798-897-5	Sequence 5, Appli
5	1000	99.1	192	2	US-08-978-523-5	Sequence 5, Appli
6	1000	99.1	193	4	US-09-155-327G-7	Sequence 7, Appli
7	1000	99.1	193	4	US-09-949-016-10928	Sequence 10928, A
8	995	98.6	193	1	US-08-798-897-4	Sequence 4, Appli
9	995	98.6	193	2	US-08-978-523-4	Sequence 4, Appli
10	990	98.1	192	1	US-08-798-897-6	Sequence 6, Appli
11	990	98.1	192	2	US-08-978-523-6	Sequence 6, Appli
12	776	76.9	333	4	US-09-155-327G-10	Sequence 10, Appl
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14	759	75.2	365	4	US-09-010-147B-24	Sequence 24, Appl
15	432.5	42.9	411	4	US-09-639-245-2	Sequence 2, Appli
16	428.5	42.5	233	3	US-09-271-014A-6	Sequence 6, Appli
17	427.5	42.4	233	1	US-08-333-565-59	Sequence 59, Appl
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19	427.5	42.4	233	1	US-08-607-269-24	Sequence 24, Appl
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26	427.5	42.4	233	3	US-09-323-743-2	Sequence 2, Appli
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30	427.5	42.4	233	5	PCT-US94-07089-7	Sequence 7, Appli
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38	411.5	40.8	239	1	US-08-112-208C-10	Sequence 10, Appl
39	411.5	40.8	239	1	US-08-248-819A-10	Sequence 10, Appl
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ALIGNMENTS

RESULT 1
US-09-155-327G-9
; Sequence 9, Application US/09155327G
; Patent No. 6790637
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 2096584
; CURRENT APPLICATION NUMBER: US/09/155,327G
; CURRENT FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mouse
US-09-155-327G-9

Query Match 100.0%; Score 1009; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 3e-107;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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RESULT 2
US-08-798-897-3
; Sequence 3, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue

```
;     NUMBER OF SEQUENCES:  53
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;       STREET:  1100 New York Avenue, N.W., Suite 600
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/798,897
;       FILING DATE:  February 11, 1997
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Esmond, Robert W.
;       REGISTRATION NUMBER:  32,893
;       REFERENCE/DOCKET NUMBER:  1483.0140001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  193 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-798-897-3

  Query Match             99.6%;  Score 1005;  DB 1;  Length 193;
  Best Local Similarity   99.5%;  Pred. No. 8.5e-107;
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Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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Db        181 GALVTVGAFFASK 193


RESULT 3
US-08-978-523-3
; Sequence 3, Application US/08978523
; Patent No. 5883229
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,523
;      FILING DATE:  herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  193 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-978-523-3

  Query Match             99.6%;  Score 1005;  DB 2;  Length 193;
  Best Local Similarity   99.5%;  Pred. No. 8.5e-107;
  Matches  192;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 4
US-08-798-897-5
; Sequence 5, Application US/08798897
; Patent No. 5789201
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
```

```
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  192 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-798-897-5

  Query Match             99.1%;  Score 1000;  DB 1;  Length 192;
  Best Local Similarity   99.5%;  Pred. No. 3.2e-106;
  Matches  191;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60

Qy         62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120

Qy        122 VQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

Qy        182 ALVTVGAFFASK 193
              ||||||||||||
Db        181 ALVTVGAFFASK 192


RESULT 5
US-08-978-523-5
; Sequence 5, Application US/08978523
; Patent No. 5883229
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,523
;      FILING DATE:  herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  192 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-978-523-5

  Query Match             99.1%;  Score 1000;  DB 2;  Length 192;
  Best Local Similarity   99.5%;  Pred. No. 3.2e-106;
  Matches  191;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60

Qy         62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120

Qy        122 VQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

Qy        182 ALVTVGAFFASK 193
              ||||||||||||
Db        181 ALVTVGAFFASK 192


RESULT 6
US-09-155-327G-7
; Sequence 7, Application US/09155327G
; Patent No. 6790637
; GENERAL INFORMATION:
;  APPLICANT: AMRAD Operations Pty Ltd
;  TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
;  TITLE OF INVENTION:  FAMILY OF APOPTOSIS-CONTROLLING GENES
;  FILE REFERENCE: 2096584
;  CURRENT APPLICATION NUMBER: US/09/155,327G
;  CURRENT FILING DATE:  1999-03-29
;  PRIOR APPLICATION NUMBER: PN8965
;  PRIOR FILING DATE: 1996-03-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: HUMAN
US-09-155-327G-7

  Query Match             99.1%;  Score 1000;  DB 4;  Length 193;
  Best Local Similarity   99.0%;  Pred. No. 3.2e-106;
  Matches  191;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 7
US-09-949-016-10928
```

; Sequence 10928, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10928
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10928

Query Match 99.1%; Score 1000; DB 4; Length 193;
Best Local Similarity 99.0%; Pred. No. 3.2e-106;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193
```

RESULT 8
US-08-798-897-4
; Sequence 4, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-798-897-4

Query Match 98.6%; Score 995; DB 1; Length 193;
Best Local Similarity 98.4%; Pred. No. 1.2e-105;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193
```

RESULT 9
US-08-978-523-4
; Sequence 4, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid

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;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-978-523-4

  Query Match             98.6%;  Score 995;  DB 2;  Length 193;
  Best Local Similarity   98.4%;  Pred. No. 1.2e-105;
  Matches  190;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 10
US-08-798-897-6
; Sequence 6, Application US/08798897
; Patent No. 5789201
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  192 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-798-897-6

  Query Match             98.1%;  Score 990;  DB 1;  Length 192;
  Best Local Similarity   98.4%;  Pred. No. 4.4e-105;
  Matches  189;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
              ||||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||

Db          1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60

Qy         62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120

Qy        122 VQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
              ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

Qy        182 ALVTVGAFFASK 193
              ||||||||||||
Db        181 ALVTVGAFFASK 192


RESULT 11
US-08-978-523-6
; Sequence 6, Application US/08978523
; Patent No. 5883229
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,523
;      FILING DATE:  herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  192 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-978-523-6

  Query Match             98.1%;  Score 990;  DB 2;  Length 192;
  Best Local Similarity   98.4%;  Pred. No. 4.4e-105;
  Matches  189;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
              ||||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||

Db          1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60

Qy         62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120

Qy        122 VQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
              ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

Qy        182 ALVTVGAFFASK 193
              ||||||||||||
Db        181 ALVTVGAFFASK 192
```

```
                ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

Qy        182 ALVTVGAFFASK 193
              ||||||||||||
Db        181 ALVTVGAFFASK 192


RESULT 12
US-09-155-327G-10
; Sequence 10, Application US/09155327G
; Patent No. 6790637
; GENERAL INFORMATION:
;  APPLICANT: AMRAD Operations Pty Ltd
;  TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
;  TITLE OF INVENTION:  FAMILY OF APOPTOSIS-CONTROLLING GENES
;  FILE REFERENCE: 2096584
;  CURRENT APPLICATION NUMBER: US/09/155,327G
;  CURRENT FILING DATE:  1999-03-29
;  PRIOR APPLICATION NUMBER: PN8965
;  PRIOR FILING DATE: 1996-03-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 333
;   TYPE: PRT
;   ORGANISM: murine
US-09-155-327G-10

  Query Match           76.9%;  Score 776;  DB 4;  Length 333;
  Best Local Similarity  75.4%;  Pred. No. 3e-80;
  Matches  159;  Conservative    5;  Mismatches   17;  Indels   30;  Gaps    4;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYG--DGALEEARRLRE-------------- 164
              |||||||||||||||||||||| |  |:        ||| :|:|
Db        121 QVQDWMVAYLETRLADWIHSSGGW-ELEAIKARVREMEEEAEKLKELQNEVEKQMNMSPP 179

Qy        165 -GN------------WASVRTVLTGAVALGA 182
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Db        180 PGNAGPVIMSLEEKMEADARSIYVGNVDYGA 210


RESULT 13
US-09-149-476-696
; Sequence 696, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P1
;  CURRENT APPLICATION NUMBER: US/09/149,476
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: PCT/US98/04493
;  EARLIER FILING DATE: 1998-03-06
;  EARLIER APPLICATION NUMBER: 60/040,162
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,333
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/038,621
;  EARLIER FILING DATE: 1997-03-07
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;  EARLIER APPLICATION NUMBER: 60/047,600
;  EARLIER FILING DATE: 1997-05-23
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;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,597
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,502
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,633
;  EARLIER FILING DATE: 1997-05-23
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;  EARLIER FILING DATE: 1997-05-23
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;  EARLIER FILING DATE: 1997-05-23
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;  EARLIER FILING DATE: 1997-05-23
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;  EARLIER APPLICATION NUMBER: 60/047,500
;  EARLIER FILING DATE: 1997-05-23
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;  EARLIER APPLICATION NUMBER: 60/047,492
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,598
;  EARLIER FILING DATE: 1997-05-23
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;  EARLIER FILING DATE: 1997-05-23
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;  EARLIER APPLICATION NUMBER: 60/047,612
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;  EARLIER APPLICATION NUMBER: 60/047,632
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,601
;  EARLIER FILING DATE: 1997-05-23
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;  EARLIER FILING DATE: 1997-04-11
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;  EARLIER APPLICATION NUMBER: 60/048,974
;  EARLIER FILING DATE: 1997-06-06
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; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,889
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; EARLIER APPLICATION NUMBER: 60/056,893
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; EARLIER APPLICATION NUMBER: 60/056,878
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; EARLIER APPLICATION NUMBER: 60/056,903
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; EARLIER APPLICATION NUMBER: 60/056,892
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; EARLIER APPLICATION NUMBER: 60/057,761
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; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,862
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; EARLIER APPLICATION NUMBER: 60/056,887
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; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 75.2%; Score 759; DB 4; Length 365;
Best Local Similarity 98.6%; Pred. No. 3e-78;
Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGW 144
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Db        121 QVQEWMVAYLETRLADWIHSSGGW 144
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RESULT 14
US-09-010-147B-24
; Sequence 24, Application US/09010147B
; Patent No. 6653445
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Human Proteins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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;             APPLICATION NUMBER: US/09/010,147B
;             FILING DATE: 12-No. 6653445-2002
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 60/034,205
;             FILING DATE: 21-JAN-1997
;             APPLICATION NUMBER: US 60/034,204
;             FILING DATE: 21-JAN-1997
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Jonathan L. Klein
;             REGISTRATION NUMBER: 41,119
;             REFERENCE/DOCKET NUMBER: PF353
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 301-309-8504
;             TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 365 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-010-147B-24

  Query Match             75.2%;  Score 759;  DB 4;  Length 365;
  Best Local Similarity   98.6%;  Pred. No. 3e-78;
  Matches  142;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGW 144
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Db        121 QVQEWMVAYLETRLADWIHSSGGW 144


RESULT 15
US-09-639-245-2
; Sequence 2, Application US/09639245
; Patent No. 6737511
; GENERAL INFORMATION:
;  APPLICANT:  Youle et al.
;  TITLE OF INVENTION:  RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL
;  TITLE OF INVENTION:  FUSION PROTEIN INHIBITS APOPTOSIS
;  FILE REFERENCE:  4239-55417
;  CURRENT APPLICATION NUMBER: US/09/639,245
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER:  60/149,220
;  PRIOR FILING DATE:  1999-08-16
;  NUMBER OF SEQ ID NOS:  8
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 411
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: genetic fusion
US-09-639-245-2

  Query Match             42.9%;  Score 432.5;  DB 4;  Length 411;
  Best Local Similarity   39.9%;  Pred. No. 8.2e-41;
  Matches   93;  Conservative   26;  Mismatches   63;  Indels   51;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGY-------------------------VCGAGP----GEGPAA 39
              | || ||: ||| ||||                         |     : ||
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Qy         40 D------------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                 :                 : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db         86 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 145

Qy         82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
              | :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :
Db        146 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQEN 205

Qy        142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGALVTVGAFFAS 192
              |||  |  |||: |  |:|: :|    |      : | | ||:| :  |: |:
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Search completed: April 10, 2005, 22:45:27
Job time : 19.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 10, 2005, 20:17:32 ; Search time 59 Seconds
(without alignments)
1675.106 Million cell updates/sec

Title: US-09-925-674B-9
Perfect score: 1009
Sequence: 1 MATPASTPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1009	100.0	193	1	BCLW_MOUSE	P70345 mus musculu
2	1005	99.6	193	2	O88996	O88996 rattus norv
3	1005	99.6	219	2	Q7TS60	Q7ts60 rattus norv
4	1000	99.1	193	1	BCLW_HUMAN	Q92843 homo sapien
5	996	98.7	192	2	Q6A093	Q6a093 mus musculu
6	960	95.1	193	2	Q8CGL4	Q8cgl4 mus musculu
7	770	76.3	178	2	Q8CFR2	Q8cfr2 mus musculu
8	770	76.3	178	2	Q9CYW5	Q9cyw5 mus musculu
9	655.5	65.0	188	2	Q6GP82	Q6gp82 xenopus lae
10	650.5	64.5	228	1	AR1_XENLA	Q91827 xenopus lae
11	439.5	43.6	233	2	Q9MYW4	Q9myw4 oryctolagus
12	432.5	42.9	229	1	BCLX_CHICK	Q07816 gallus gall
13	432.5	42.9	233	2	Q8SQ42	Q8sq42 felis silve
14	431.5	42.8	233	1	BCLX_PIG	O77737 sus scrofa
15	431.5	42.8	233	2	Q9N1A2	Q9n1a2 sus scrofa
16	428.5	42.5	233	1	BCLX_MOUSE	Q64373 mus musculu
17	428.5	42.5	233	1	BCLX_RAT	P53563 rattus norv
18	428.5	42.5	233	2	Q9MZS7	Q9mzs7 ovis aries
19	427.5	42.4	233	1	BCLX_HUMAN	Q07817 homo sapien
20	427.5	42.4	233	2	Q76LT7	Q76lt7 canis famil
21	423.5	42.0	233	1	BCL2_CHICK	Q00709 gallus gall
22	415.5	41.2	229	1	BCL2_BOVIN	O02718 bos taurus
23	413	40.9	236	1	BCL2_RAT	P49950 rattus norv
24	412	40.8	236	1	BCL2_MOUSE	P10417 mus musculu
25	412	40.8	236	2	Q7TSN8	Q7tsn8 rattus norv
26	412	40.8	236	2	Q8BQK4	Q8bqk4 mus musculu
27	411.5	40.8	239	1	BCL2_HUMAN	P10415 homo sapien
28	406	40.2	79	2	Q7TS61	Q7ts61 rattus norv
29	402	39.8	236	1	BCL2_CRILO	Q9jjv8 cricetulus
30	401.5	39.8	239	2	Q75SV7	Q75sv7 canis famil
31	401	39.7	180	2	Q9BDD5	Q9bdd5 bos taurus
32	401	39.7	217	2	Q99N35	Q99n35 mus musculu
33	400	39.6	238	2	Q90Z98	Q90z98 brachydanio
34	398.5	39.5	180	2	Q9BDX7	Q9bdx7 bos taurus
35	398	39.4	236	2	Q923R6	Q923r6 cricetulus
36	396.5	39.3	201	2	Q6GLI5	Q6gli5 xenopus tro
37	395.5	39.2	235	2	Q8I008	Q8i008 felis silve
38	395	39.1	236	2	Q6R755	Q6r755 canis famil
39	380.5	37.7	284	2	Q7TS62	Q7ts62 rattus norv
40	374.5	37.1	188	2	Q9QWX2	Q9qwx2 mus musculu
41	374.5	37.1	235	2	O35843	O35843 mus musculu
42	372.5	36.9	188	2	Q9H1R6	Q9h1r6 homo sapien
43	371	36.8	204	2	Q90ZH2	Q90zh2 xenopus lae
44	369	36.6	204	1	AR11_XENLA	Q91828 xenopus lae
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ALIGNMENTS

RESULT 1
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ID BCLW_MOUSE STANDARD; PRT; 193 AA.
AC P70345;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apoptosis regulator Bcl-W (Bcl-2-like 2 protein).
GN Name=Bcl2l2; Synonyms=Bclw;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL Oncogene 13:665-675(1996).
RN [2]
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RC STRAIN=C57BL/10J;
RX MEDLINE=98160183; PubMed=9500547;
RA Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,
RA Russell L.D., Macgregor G.R.;
RT "Testicular degeneration in Bclw-deficient mice.";
RL Nat. Genet. 18:251-256(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

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RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
CC   -!- FUNCTION: Promotes cell survival.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC       in a wide range of tissues, with highest levels in brain, colon,
CC       and salivary gland.
CC   -!- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC       function.
CC   -!- SIMILARITY: Belongs to the Bcl-2 family.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U59746; AAB09056.1; -.
DR   EMBL; AF030769; AAB86430.1; -.
DR   EMBL; AK015644; BAB29912.1; -.
DR   HSSP; Q92843; 100L.
DR   MGD; MGI:108052; Bcl212.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006915; P:apoptosis; IDA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis.
FT   DOMAIN        9     29       BH4.
FT   DOMAIN       85    104       BH1.
FT   DOMAIN      136    151       BH2.
SQ   SEQUENCE   193 AA;  20790 MW;  36CA185F5945DFB4 CRC64;

  Query Match          100.0%;  Score 1009;  DB 1;  Length 193;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-82;
  Matches  193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
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Db        181 GALVTVGAFFASK 193


RESULT 2
O88996
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ID   O88996      PRELIMINARY;      PRT;   193 AA.
AC   O88996;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Bcl-w (Hypothetical protein).
GN   Name=bcl-w;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=99292146; PubMed=10366024; DOI=10.1016/S0306-4522(98)00642-3;
RA   Hamner S., Skoglosa Y., Lindholm D.;
RT   "Differential expression of bcl-w and bcl-x messenger RNA in the
RT   developing and adult rat nervous system.";
RL   Neuroscience 91:673-684(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=22672518; PubMed=12787069;
RA   Itoh T., Itoh A., Pleasure D.;
RT   "Bcl-2-related protein family gene expression during oligodendroglial
RT   differentiation.";
RL   J. Neurochem. 85:1500-1512(2003).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF096291; AAC64200.1; -.
DR   EMBL; AY185098; AAO64468.1; -.
DR   EMBL; BC074021; AAH74021.1; -.
DR   HSSP; Q92843; 100L.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
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KW   Hypothetical protein.
SQ   SEQUENCE   193 AA;  20820 MW;  36D6742F4529AFB4 CRC64;

  Query Match             99.6%;  Score 1005;  DB 2;  Length 193;
  Best Local Similarity   99.5%;  Pred. No. 5.8e-82;
  Matches  192;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 3
Q7TS60
ID   Q7TS60      PRELIMINARY;      PRT;   219 AA.
AC   Q7TS60;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   BCL-WEL.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=22672518; PubMed=12787069;
RA   Itoh T., Itoh A., Pleasure D.;
RT   "Bcl-2-related protein family gene expression during oligodendroglial
RT   differentiation.";
RL   J. Neurochem. 85:1500-1512(2003).
DR   EMBL; AY185100; AAO64470.1; -.
DR   HSSP; Q07817; 1R2D.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   219 AA;  23720 MW;  30E36041BC1DC66F CRC64;

  Query Match             99.6%;  Score 1005;  DB 2;  Length 219;
  Best Local Similarity   99.5%;  Pred. No. 6.7e-82;
  Matches  192;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 86

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 146

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 206

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        207 GALVTVGAFFASK 219


RESULT 4
BCLW_HUMAN
ID   BCLW_HUMAN     STANDARD;      PRT;   193 AA.
AC   Q92843;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Apoptosis regulator Bcl-W (Bcl-2-like 2 protein).
GN   Name=BCL2L2; Synonyms=BCLW, KIAA0271;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96358615; PubMed=8761287;
RA   Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
RA   Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT   "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL   Oncogene 13:665-675(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97191544; PubMed=9039502;
RA   Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,
RA   Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT   "Prediction of the coding sequences of unidentified human genes. VI.
RT   The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT   analysis of cDNA clones from cell line KG-1 and brain.";
RL   DNA Res. 3:321-329(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Promotes cell survival.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC       in a wide range of tissues, with highest levels in brain, colon,
CC       and salivary gland.
CC   -!- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC       function.
CC   -!- SIMILARITY: Belongs to the Bcl-2 family.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
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CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U59747; AAB09055.1; -.
DR   EMBL; D87461; BAA19666.2; ALT_INIT.
DR   EMBL; BC021198; AAH21198.1; -.
DR   PDB; 1MK3; NMR; A=2-172.
DR   PDB; 1O0L; NMR; A=1-183.
DR   Genew; HGNC:995; BCL2L2.
DR   H-InvDB; HIX0011536; -.
DR   MIM; 601931; -.
DR   GO; GO:0005737; C:cytoplasm; NAS.
DR   GO; GO:0006916; P:anti-apoptosis; TAS.
DR   GO; GO:0007283; P:spermatogenesis; TAS.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   3D-structure; Apoptosis.
FT   DOMAIN        9     29       BH4.
FT   DOMAIN       85    104       BH1.
FT   DOMAIN      136    151       BH2.
SQ   SEQUENCE   193 AA;  20774 MW;  3792243A50281761 CRC64;

  Query Match             99.1%;  Score 1000;  DB 1;  Length 193;
  Best Local Similarity   99.0%;  Pred. No. 1.6e-81;
  Matches  191;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 5
Q6A093
ID   Q6A093      PRELIMINARY;      PRT;   192 AA.
AC   Q6A093;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   MKIAA0271 protein (Fragment).
GN   Name=mKIAA0271;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA   Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA   Nagase T., Ohara O., Koga H.;
RT   "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT   IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
RT   cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT   Randomly Sampled from Size-Fractionated Libraries.";
RL   DNA Res. 11:205-218(2004).
DR   EMBL; AK172925; BAD32203.1; -.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006915; P:apoptosis; IDA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
FT   NON_TER       1     1
SQ   SEQUENCE   192 AA;  20763 MW;  A56CE4EC51D41F8A CRC64;

  Query Match             98.7%;  Score 996;  DB 2;  Length 192;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-81;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 61

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 121

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 181

Qy        181 GALVTVGAFF 190
              ||||||||||
Db        182 GALVTVGAFF 191


RESULT 6
Q8CGL4
ID   Q8CGL4      PRELIMINARY;      PRT;   193 AA.
AC   Q8CGL4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Bcl2-like protein 2.
GN   Name=Bcl2l2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL; TISSUE=Skin;
RA   Su H.-Y., Cheng W.T.K., Chen S.C., Lin C.T., Lien Y.Y., Liu H.J.,
RA   Gilmour R.S.;
RT   "Mouse keratinocytes express c98, a novel gene homologous to bcl-2,
RT   that is stimulated by insulin-like growth factor 1 and prevents
RT   dexamethasone-induced apoptosis.";
RL   Biochim. Biophys. Acta 1676:127-137(2004).
DR   EMBL; AY170344; AAO13177.2; -.
DR   HSSP; Q92843; 1O0L.
DR   MGD; MGI:108052; Bcl2l2.
```

```
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006915; P:apoptosis; IDA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
SQ   SEQUENCE   193 AA;  20958 MW;  60D7F9E4DC56DFAE CRC64;

  Query Match             95.1%;  Score 960;  DB 2;  Length 193;
  Best Local Similarity   95.9%;  Pred. No. 6.2e-78;
  Matches  185;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||| ||||:|||||||||||||||||||||||||| :||||||
Db          1 MATPASTPDTRALVAYFVGYQLRQKGYVCGAGPGEGPAADPLHQAMRAAGDELQTRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              || |||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 FSHLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKHMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVAYLETRLAYWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||  |
Db        181 GALVTVGAFFAYK 193


RESULT 7
Q8CFR2
ID   Q8CFR2      PRELIMINARY;      PRT;   178 AA.
AC   Q8CFR2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Bcl212 protein.
GN   Name=Bcl212;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC040369; AAH40369.1; -.
DR   HSSP; Q92843; 1O0L.
DR   MGD; MGI:108052; Bcl212.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006915; P:apoptosis; IDA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   178 AA;  19119 MW;  E2C3F3F79528E9D7 CRC64;

  Query Match             76.3%;  Score 770;  DB 2;  Length 178;
  Best Local Similarity   96.7%;  Pred. No. 5.9e-61;
  Matches  145;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTAL 150
              |||||||||||||||||||||||||   : |
Db        121 QVQDWMVAYLETRLADWIHSSGGWVRSSQL 150


RESULT 8
Q9CYW5
ID   Q9CYW5      PRELIMINARY;      PRT;   178 AA.
AC   Q9CYW5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
DE   enriched library, clone:2810435A13 product:Bcl2-like 2, full insert
DE   sequence.
GN   Name=Bcl212;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
```

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RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK013244; BAB28740.1; -.
DR   HSSP; Q92843; 1O0L.
DR   MGD; MGI:108052; Bcl2l2.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006915; P:apoptosis; IDA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   178 AA;  19147 MW;  E2D4C3F79528E9D7 CRC64;

  Query Match          76.3%;  Score 770;  DB 2;  Length 178;
  Best Local Similarity  96.7%;  Pred. No. 5.9e-61;
  Matches  145;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTAL 150
              |||||||||||||||||||||||||||||  : |
Db        121 QVQDWMVAYLETRLADWIHSSGGWVRSSQL 150


RESULT 9
Q6GP82
ID   Q6GP82       PRELIMINARY;      PRT;   188 AA.
AC   Q6GP82;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MGC80617 protein.
GN   Name=MGC80617;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073259; AAH73259.1; -.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
SQ   SEQUENCE   188 AA;  20441 MW;  CB3C1A8C55F16B96 CRC64;

  Query Match          65.0%;  Score 655.5;  DB 2;  Length 188;
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  Best Local Similarity   69.4%;  Pred. No. 1.1e-50;
  Matches  127;  Conservative   19;  Mismatches   34;  Indels    3;  Gaps    1;

Qy         11 RALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHV 70
              ||||  |||  |||  |:  |        |||:  ||  |||||||||| |||: ||::: |:||
Db          9 RALVEDFVRYKLCQRSLV---PEPAGPASCALHSAMRAAGDEFEERFRQAFSEISTQIHV 65

Qy         71 TPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYL 130
              |||:|  ||  :|:  ||||| ||||:|||||||||||||||||||| ||: ::||||| ||
Db         66 TPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTYL 125

Qy        131 ETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFF 190
              || |  || |:|||  |  ||||||:|||||  |||||||::||||||||||||:|||| |
Db        126 ETNLRGWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGALF 185

Qy        191 ASK 193
              |||
Db        186 ASK 188


RESULT 10
AR1_XENLA
ID   AR1_XENLA      STANDARD;      PRT;   228 AA.
AC   Q91827;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   29-MAR-2004 (Rel. 43, Last annotation update)
DE   Apoptosis regulator R1 (XR1) (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Head;
RX   MEDLINE=95331613; PubMed=7607538; DOI=10.1016/0378-1119(95)00159-4;
RA   Cruz-Reyes J., Tata J.R.;
RT   "Cloning, characterization and expression of two Xenopus bcl-2-like
RT   cell-survival genes.";
RL   Gene 158:171-179(1995).
CC   -!- FUNCTION: Could be the homolog of mammalian Bcl-W.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC   -!- DEVELOPMENTAL STAGE: Developmental regulation only occurs in the
CC       brain of mid-metamorphosic to post-metamorphosic tadpoles and
CC       adults, where an increase of several fold has been observed.
CC   -!- SIMILARITY: Belongs to the Bcl-2 family.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X82462; CAA57845.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
KW   Apoptosis; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN      120    139       BH1.
FT   DOMAIN      171    186       BH2.
FT   TRANSMEM    207    227       Potential.
SQ   SEQUENCE   228 AA;  25068 MW;  C499D449A585F8A9 CRC64;

  Query Match             64.5%;  Score 650.5;  DB 1;  Length 228;
  Best Local Similarity   68.5%;  Pred. No. 3.9e-50;
  Matches  126;  Conservative   20;  Mismatches   35;  Indels    3;  Gaps    1;

Qy         10 TRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLH 69
              :|||| | | ||| |:  |        | |:  || |||||||||| |||: ||::: |:|
Db         48 SRALVEDLVRYKLCQRSLV---PEPSGAASCALHSAMRAAGDEFEERFRQAFSEISTQIH 104

Qy         70 VTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAY 129
              ||||:|  || :|:  ||||| ||||:|||||||||||||||||| ||: ::||||| |
Db        105 VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY 164

Qy        130 LETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAF 189
              ||| | ||| |:|||  |  |||||||:||||| |||||||::||||||||||:||||
Db        165 LETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL 224

Qy        190 FASK 193
              ||||
Db        225 FASK 228


RESULT 11
Q9MYW4
ID   Q9MYW4      PRELIMINARY;      PRT;   233 AA.
AC   Q9MYW4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Bcl-X.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Knott J.C., Robertson L., James E.R.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY005131; AAF88137.1; -.
DR   HSSP; P53563; 1AF3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR004725; Bcl2_reg.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   TIGRFAMs; TIGR00865; bcl-2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   233 AA;  25986 MW;  12F0F30344D53F93 CRC64;

  Query Match             43.6%;  Score 439.5;  DB 2;  Length 233;
  Best Local Similarity   42.0%;  Pred. No. 3.2e-31;
  Matches   94;  Conservative   22;  Mismatches   57;  Indels   51;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGYVC--------------GAG---------------PGEGPAA 39
              | || ||: ||| ||||                 | |               | : ||
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTGPEMETPSAINGNPAWHPADSPAV 65

Qy         40 D-----------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
              :                 : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db         66 NGATGHSSSLDAREVIPMTAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125

Qy         82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
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                | :|||: | ||||:|||| || ||| |||:|||| || ::  ||  ||   |  ||  :
Db        126 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMEVLVSRIAAWMATYLNDHLEPWIQEN 185

Qy        142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
              |||  |  |||: |  |:|: :|    |      : | | ||:|
Db        186 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT 12
BCLX_CHICK
ID   BCLX_CHICK     STANDARD;      PRT;   229 AA.
AC   Q07816; Q98908;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
GN   Name=BCL2L1; Synonyms=BCL-X, BCLX;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RX   MEDLINE=93364977; PubMed=8358789; DOI=10.1016/0092-8674(93)90508-N;
RA   Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA   Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT   "bcl-x, a bcl-2-related gene that functions as a dominant regulator of
RT   apoptotic cell death.";
RL   Cell 74:597-608(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM LONG).
RC   STRAIN=Hubbard White Mountain; TISSUE=Testis;
RX   MEDLINE=97264485; PubMed=9110311;
RX   DOI=10.1002/(SICI)1098-2795(199705)47:1<26::AID-MRD4>3.3.CO;2-V;
RA   Vilagrasa X., Mezquita C., Mezquita J.;
RT   "Differential expression of bcl-2 and bcl-x during chicken
RT   spermatogenesis.";
RL   Mol. Reprod. Dev. 47:26-29(1997).
CC   -!- FUNCTION: Dominant regulator of apoptotic cell death. The long
CC       form displays cell death repressor activity, whereas the short
CC       isoform promotes apoptosis (By similarity).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC       envelope (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Long;
CC         IsoId=Q07816-1; Sequence=Displayed;
CC       Name=Short;
CC         IsoId=Q07816-2; Sequence=VSP_000514;
CC   -!- TISSUE SPECIFICITY: Highest expression in organs with lymphoid
CC       development.
CC   -!- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC       function. Intact BH1 and BH2 domains are required for anti-
CC       apoptotic activity (By similarity).
CC   -!- SIMILARITY: Belongs to the Bcl-2 family.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Z23110; CAA80657.1; -.
DR   EMBL; U26645; AAB07677.1; -.
DR   PIR; A47537; A47537.
DR   HSSP; P53563; 1AF3.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR004725; Bcl2_reg.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   TIGRFAMs; TIGR00865; bcl-2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Alternative splicing; Apoptosis; Transmembrane.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       82     96       BH3.
FT   DOMAIN      125    144       BH1.
FT   DOMAIN      176    191       BH2.
FT   TRANSMEM    206    223       Potential.
FT   VARSPLIC    185    229       ERFVDLYGNNAAAELRKGQETFNKWLLTGATVAGVLLLGSL
FT                                LSRK -> VRTALP (in isoform Short).
FT                                /FTId=VSP_000514.
SQ   SEQUENCE   229 AA;  25733 MW;  A97D3A4D04C0E9DA CRC64;

  Query Match             42.9%;  Score 432.5;  DB 1;  Length 229;
  Best Local Similarity   41.7%;  Pred. No. 1.3e-30;
  Matches   95;  Conservative   22;  Mismatches   62;  Indels   49;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGY----------------------VCGAGPGEGP---------- 37
                | || ||| ||| |:|:                      |    |   |
Db          6 RELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65

Qy         38 ------------AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                          |  : ||:| |||||| |:|| |||| :|||:|||:| | | || :|
Db         66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE 125

Qy         86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWA 145
              ||  | ||||:|||| || ||| |||:|||  |||::  ||  ||   |  ||  :|||
Db        126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWE 185

Qy        146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
               |  |||: |   |  ||:|     : :||||   | |: :|:  : |
Db        186 RFVDLYGNNA---AAELRKGQETFNKWLLTGATVAGVLL-LGSLLSRK 229


RESULT 13
Q8SQ42
ID   Q8SQ42      PRELIMINARY;      PRT;   233 AA.
AC   Q8SQ42;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Bcl-xl protein.
GN   Name=bcl-xl;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Nagafuchi S., Sano J., Kano R., Hasegawa A.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB080951; BAB85856.2; -.
DR   HSSP; Q07817; 1MAZ.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR004725; Bcl2_reg.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
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DR   SMART; SM00265; BH4; 1.
DR   TIGRFAMs; TIGR00865; bcl-2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   233 AA;  26017 MW;  CD17F24FE9D47BC9 CRC64;

  Query Match             42.9%;  Score 432.5;  DB 2;  Length 233;
  Best Local Similarity   41.6%;  Pred. No. 1.3e-30;
  Matches   97;  Conservative   23;  Mismatches   58;  Indels   55;  Gaps    5;

Qy         11 RALVADFVGYKLRQKGY----------------------------------------V 28
              | || ||: ||| ||||                                        |
Db          6 RELVVDFLSYKLSQKGYSWSRFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy         29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
               ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db         66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy         81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
              || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db        125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE 184

Qy        141 SGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
              :|||  |  |||: |  |:|:   |   | |  |||    | :| :|: |: |
Db        185 NGGWDTFVELYGNNAAAESRK---GQERSNRWFLTGMTVAG-VVLLGSLFSRK 233


RESULT 14
BCLX_PIG
ID   BCLX_PIG       STANDARD;      PRT;   233 AA.
AC   O77737;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
GN   Name=BCL2L1; Synonyms=BCLX, BLC2L;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99171363; PubMed=10072723; DOI=10.1006/jmcc.1998.0855;
RA   Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT   "Quantification of cardioprotective gene expression in porcine short-
RT   term hibernating myocardium.";
RL   J. Mol. Cell. Cardiol. 31:147-158(1999).
CC   -!- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-
CC       apoptotic activity is inhibited by association with SIVA isoform
CC       1.Inhibits activation of caspases (By similarity). Appears to
CC       regulate cell death by blocking the voltage-dependent anion
CC       channnel (VDAC) by binding to it and preventing the release of the
CC       caspase activator, cytochrome c, from the mitochondrial membrane.
CC   -!- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC       similarity). Heterodimerization with BAX does not seem to be
CC       required for anti-apoptotic activity (By similarity). Isoform Bcl-
CC       X(L) binds to Siva isoform 1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC       envelope (By similarity).
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC       The BH1 and BH2 domains are required for both heterodimerization
CC       with other Bcl-2 family members and for repression of cell death.
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis (By
CC       similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC       apoptotic activity (By similarity).
CC   -!- SIMILARITY: Belongs to the Bcl-2 family.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC   -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ001203; CAA04597.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR004725; Bcl2_reg.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   TIGRFAMs; TIGR00865; bcl-2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Mitochondrion; Transmembrane.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       Potential.
SQ   SEQUENCE   233 AA;  26061 MW;  18BF6FA0441912B2 CRC64;

  Query Match             42.8%;  Score 431.5;  DB 1;  Length 233;
  Best Local Similarity   41.8%;  Pred. No. 1.6e-30;
  Matches   94;  Conservative   21;  Mismatches   57;  Indels   53;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGY----------------------------------------V 28
              | || ||: ||| ||||                                        |
Db          6 RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65

Qy         29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
               ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db         66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy         81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
              || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db        125 QVLNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE 184

Qy        141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
              :|||  |  |||: |  |:|: :|    |       | | | ||:|
Db        185 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL 229


RESULT 15
Q9N1A2
ID   Q9N1A2       PRELIMINARY;      PRT;   233 AA.
AC   Q9N1A2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Anti-apoptotic regulator Bcl-xL.
GN   Name=bcl-xL;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RA   Lee T.L., Canty J.M.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF216205; AAF33212.1; -.
```

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DR   HSSP; Q07817; 1R2D.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   InterPro; IPR000712; Bcl2_BH.
DR   InterPro; IPR003093; Bcl2_BH4.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR004725; Bcl2_reg.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   TIGRFAMs; TIGR00865; bcl-2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   233 AA;  26047 MW;  2FA312818B25E17D CRC64;

  Query Match             42.8%;  Score 431.5;  DB 2;  Length 233;
  Best Local Similarity   41.8%;  Pred. No. 1.6e-30;
  Matches   94;  Conservative   21;  Mismatches   57;  Indels   53;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGY----------------------------------------V 28
              | || ||: ||| ||||                                        |
Db          6 RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65

Qy         29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
               ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db         66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy         81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
              || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db        125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE 184

Qy        141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
              :|||  |  |||: |  |:|: :|    |       | | | ||:|
Db        185 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL 229

Search completed: April 10, 2005, 22:42:54
Job time : 60 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 10, 2005, 20:12:38 ; Search time 65 Seconds
(without alignments)
1148.381 Million cell updates/sec

Title: US-09-925-674B-9
Perfect score: 1009
Sequence: 1 MATPASTPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1009	100.0	193	2	AAY05531	Aay05531 Mouse Bcl
2	1005	99.6	193	2	AAW61391	Aaw61391 Rat bcl-y
3	1005	99.6	193	2	AAW97391	Aaw97391 The rat b
4	1000	99.1	192	2	AAW97393	Aaw97393 Protein s
5	1000	99.1	193	2	AAY05530	Aay05530 Human Bcl
6	1000	99.1	193	7	ADD46742	Add46742 Human Pro
7	1000	99.1	193	8	ADP88349	Adp88349 Human Bcl
8	995	98.6	193	2	AAW61392	Aaw61392 Human bcl
9	995	98.6	193	2	AAW97392	Aaw97392 The human
10	993	98.4	193	2	AAW36047	Aaw36047 Human bcl
11	993	98.4	193	2	AAY05532	Aay05532 Human Bcl
12	990	98.1	192	2	AAW97394	Aaw97394 Mammalian
13	967.5	95.9	192	2	AAY05533	Aay05533 Mouse Bcl
14	947	93.9	183	8	ADP88350	Adp88350 Derivativ
15	876	86.8	168	2	AAW36048	Aaw36048 Mouse bcl
16	814.5	80.7	190	5	AAO18223	Aao18223 Human Bcl
17	759	75.2	365	2	AAW59884	Aaw59884 Amino aci
18	759	75.2	365	5	ABG95556	Abg95556 Human nov
19	759	75.2	365	6	ABO34750	Abo34750 Fragment
20	759	75.2	365	7	ADI23411	Adi23411 Novel hum
21	759	75.2	365	8	ADH74413	Adh74413 Human sec
22	757.5	75.1	185	8	ABM84148	Abm84148 Human dia
23	457.5	45.3	179	8	ADH52635	Adh52635 Chinese h
24	448.5	44.4	199	8	ADH52637	Adh52637 Chinese h
25	441.5	43.8	219	8	ADH52639	Adh52639 Chinese h
26	436.5	43.3	219	8	ADH52641	Adh52641 Chinese h
27	436.5	43.3	342	8	ADQ97763	Adq97763 Mouse can
28	432.5	42.9	411	4	AAU00219	Aau00219 Bcl-Xl-DT
29	431.5	42.8	233	8	ADQ80679	Adq80679 Porcine a
30	430.5	42.7	237	5	ABG78480	Abg78480 Wild type
31	429.5	42.6	233	8	ADH52633	Adh52633 Chinese h
32	428.5	42.5	233	4	AAB73303	Aab73303 Rat wild-
33	428.5	42.5	233	7	ADE62921	Ade62921 Rat Prote
34	428.5	42.5	233	7	ADE62491	Ade62491 Rat Prote
35	428.5	42.5	233	8	ADQ80678	Adq80678 Mouse ant
36	427.5	42.4	233	2	AAR68887	Aar68887 Human thy
37	427.5	42.4	233	2	AAW05821	Aaw05821 Bcl-XL pr
38	427.5	42.4	233	2	AAW31530	Aaw31530 Human ant
39	427.5	42.4	233	3	AAY69969	Aay69969 Human Bcl
40	427.5	42.4	233	3	AAY83223	Aay83223 Bcl-x pol
41	427.5	42.4	233	4	AAB50538	Aab50538 Human Bcl
42	427.5	42.4	233	4	AAG64262	Aag64262 Human Bcl
43	427.5	42.4	233	4	AAB47515	Aab47515 Protein e
44	427.5	42.4	233	7	ADE62493	Ade62493 Human Pro
45	427.5	42.4	233	7	ABW02410	Abw02410 Human bcl

ALIGNMENTS

RESULT 1
AAY05531
ID AAY05531 standard; protein; 193 AA.
XX
AC AAY05531;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse Bcl-w protein essential for spermatogenesis.
XX
KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW animal model.
XX
OS Mus sp.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
DR WPI; 1999-243890/20.
DR N-PSDB; AAX25133.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w.
XX
PS Claim 2; Page 35; 52pp; English.
XX
CC The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2
CC family which is widely expressed and which is essential for
CC spermatogenesis. The invention relates generally to a method of treatment
CC and to an animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for reducing
CC fertility, by modulating spermatogenesis. An animal model carries a
CC mutation is at least one allele of the human or murine bcl-w gene (see
CC AAX25132-35) or in a gene associated with bcl-w. Such animals have
CC disorganised seminferous tubules and are substantially infertile, but
CC possess no other major abnormalities as determined by histological
CC examination. They can be used to screen for therapeutic molecules
CC including genetic sequences capable of inducing, enhancing or otherwise

```
CC   facilitating spermatogenesis in animals, or which can induce infertility
XX
SQ   Sequence 193 AA;

  Query Match             100.0%;  Score 1009;  DB 2;  Length 193;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-102;
  Matches  193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 2
AAW61391
ID   AAW61391 standard; protein; 193 AA.
XX
AC   AAW61391;
XX
DT   02-OCT-1998  (first entry)
XX
DE   Rat bcl-y protein.
XX
KW   bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS   Rattus sp.
XX
PN   US5789201-A.
XX
PD   04-AUG-1998.
XX
PF   11-FEB-1997;   97US-00798897.
XX
PR   23-FEB-1996;   96US-0012201P.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1998-446079/38.
DR   N-PSDB; AAV28333.
XX
PT   Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
PT   recombinant protein for use in treating uncontrolled cell growth e.g.
PT   cancers.
XX
PS   Example; Fig 3A; 27pp; English.
XX
CC   The mammalian bcl-y protein is a member of the bcl-2 family, components
CC   in the cell death pathway. The bcl-2 family have both apoptotic activity
CC   and the apoptosis blocking activity. bcl-y falls in the apoptosis
CC   activity category. The recombinant protein may be used to prevent
CC   uncontrolled cell growth, either by its direct administration to
CC   recombinant genetic constructs to increase its expression in vivo. Also,
CC   antisense constructs can be used in disorders where prevention of cell
CC   death is desired
XX
SQ   Sequence 193 AA;

  Query Match             99.6%;  Score 1005;  DB 2;  Length 193;
  Best Local Similarity   99.5%;  Pred. No. 2.6e-101;
  Matches  192;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 3
AAW97391
ID   AAW97391 standard; protein; 193 AA.
XX
AC   AAW97391;
XX
DT   20-MAY-1999  (first entry)
XX
DE   The rat bcl-y protein.
XX
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
OS   Rattus sp.
XX
PN   US5883229-A.
XX
PD   16-MAR-1999.
XX
PF   25-NOV-1997;   97US-00978523.
XX
PR   23-FEB-1996;   96US-0012201P.
PR   11-FEB-1997;   97US-00798897.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1999-214150/18.
DR   N-PSDB; AAX15945.
XX
PT   Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT   modulating programmed cell death.
XX
PS   Disclosure; Col 15-18; 26pp; English.
XX
CC   The present sequence represents rat bcl-y protein (Rbcl-y). The
CC   specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
CC   Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC   programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC   proteins may be used to treat conditions associated with a disruption of
CC   the cell death pathway. If they act as cell death inhibitors, they may be
CC   used in therapies to treat subjects suffering from: strokes, head trauma,
CC   Alzheimer's Disease, neural and muscular degenerative diseases
CC   (especially multiple sclerosis), myocardial infarction, vitally induced
CC   cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC   - conditions where cells under go premature cell death as a result of
CC   triggers which may or may not be apparent. They may also be used in this
CC   way to develop cell lines which remain viable in culture for an extended
```

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CC   period. In contrast, if they act as cell death stimulators, Rbcl-y and
CC   Hbcl-y may be used to treat conditions associated with prolonged cell
CC   life span such as cancer (especially kaposi's sarcoma and lung cancer)
CC   and auto/hyperimmune diseases. They may also be used to cause cell death
CC   in, and hence control, parasites
XX
SQ   Sequence 193 AA;

  Query Match             99.6%;  Score 1005;  DB 2;  Length 193;
  Best Local Similarity   99.5%;  Pred. No. 2.6e-101;
  Matches  192;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 4
AAW97393
ID   AAW97393 standard; protein; 192 AA.
XX
AC   AAW97393;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Protein sequence of the specification.
XX
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
OS   Unidentified.
XX
PN   US5883229-A.
XX
PD   16-MAR-1999.
XX
PF   25-NOV-1997;   97US-00978523.
XX
PR   23-FEB-1996;   96US-0012201P.
PR   11-FEB-1997;   97US-00798897.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1999-214150/18.
XX
PT   Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT   modulating programmed cell death.
XX
PS   Disclosure; Col 19-20; 26pp; English.
XX
CC   The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
CC   protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
CC   thought to be involved in programmed cell death (apoptosis and necrosis).
CC   Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
CC   with a disruption of the cell death pathway. If they act as cell death
CC   inhibitors, they may be used in therapies to treat subjects suffering
CC   from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC   degenerative diseases (especially multiple sclerosis), myocardial
CC   infarction, vitally induced cell death, aging, spinal cord injuries and
CC   amyotrophic lateral sclerosis- conditions where cells under go premature
CC   cell death as a result of triggers which may or may not be apparent. They
CC   may also be used in this way to develop cell lines which remain viable in
CC   culture for an extended period. In contrast, if they act as cell death
CC   stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated
CC   with prolonged cell life span such as cancer (especially kaposi's sarcoma
CC   and lung cancer) and auto/hyperimmune diseases. They may also be used to
CC   cause cell death in, and hence control, parasites
XX
SQ   Sequence 192 AA;

  Query Match             99.1%;  Score 1000;  DB 2;  Length 192;
  Best Local Similarity   99.5%;  Pred. No. 8.9e-101;
  Matches  191;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60

Qy         62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120

Qy        122 VQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

Qy        182 ALVTVGAFFASK 193
              ||||||||||||
Db        181 ALVTVGAFFASK 192


RESULT 5
AAY05530
ID   AAY05530 standard; protein; 193 AA.
XX
AC   AAY05530;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Human Bcl-w protein essential for spermatogenesis.
XX
KW   Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW   animal model.
XX
OS   Homo sapiens.
XX
PN   WO9913710-A1.
XX
PD   25-MAR-1999.
XX
PF   16-SEP-1998;   98WO-AU000764.
XX
PR   16-SEP-1997;   97AU-00009228.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Cory S,  Adams J,  Print C,  Gibson L,  Koentgen F;
XX
DR   WPI; 1999-243890/20.
DR   N-PSDB; AAX25132.
XX
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w.
XX
PS   Claim 2; Page 33; 52pp; English.
XX
CC   The present sequence is human Bcl-w, a pro-survival member of the Bcl-2
```

CC family which is widely expressed and which is essential for
CC spermatogenesis. The invention relates generally to a method of treatment
CC and to an animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for reducing
CC fertility, by modulating spermatogenesis. An animal model carries a
CC mutation is at least one allele of the human or murine bcl-w gene (see
CC AAX25132-35) or in a gene associated with bcl-w. Such animals have
CC disorganised seminferous tubules and are substantially infertile, but
CC possess no other major abnormalities as determined by histological
CC examination. They can be used to screen for therapeutic molecules
CC including genetic sequences capable of inducing, enhancing or otherwise
CC facilitating spermatogenesis in animals, or which can induce infertility
XX
SQ Sequence 193 AA;

Query Match 99.1%; Score 1000; DB 2; Length 193;
Best Local Similarity 99.0%; Pred. No. 9e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193
```

RESULT 6
ADD46742
ID ADD46742 standard; protein; 193 AA.
XX
AC ADD46742;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein Q92843, SEQ ID NO 12427.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q92843.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 193 AA;

Query Match 99.1%; Score 1000; DB 7; Length 193;
Best Local Similarity 99.0%; Pred. No. 9e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193
```

RESULT 7
ADP88349
ID ADP88349 standard; protein; 193 AA.
XX
AC ADP88349;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human Bcl-w protein.
XX
KW Bcl-w; human; protein structure; protein co-ordinate data.
XX
OS Homo sapiens.
XX
PN WO2004050697-A1.
XX
PD 17-JUN-2004.

```
XX
PF   03-DEC-2003; 2003WO-AU001624.
XX
PR   03-DEC-2002; 2002AU-00953259.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Hinds MG,  Huang DCS,  Day CL;
XX
DR   WPI; 2004-487529/46.
XX
PT   Solution useful for identifying or selecting agents that are capable of
PT   inhibiting biological activity of Bcl-w, comprises molecule that has Bcl-
PT   w active site defined by specific structure coordinates of Bcl-w amino
PT   acid residues.
XX
PS   Disclosure; Page 804-805; 810pp; English.
XX
CC   The present invention relates to a solution comprising a molecule or
CC   molecular complex that comprises at least a fragment of Bcl-w. Also
CC   disclosed is the structure of Bcl-w, in the form of protein coordinate
CC   data. The solution is useful for identifying, selecting or designing
CC   agents that are capable of inhibiting or potentiating one or more
CC   biological activity of Bcl-w, and in solving the structures of other
CC   proteins with similar structure. It is also useful for characterizing the
CC   three-dimensional structure of the Bcl-w molecule, molecular complex or
CC   its derivative. The present sequence is the human Bcl-w protein.
XX
SQ   Sequence 193 AA;

  Query Match             99.1%;  Score 1000;  DB 8;  Length 193;
  Best Local Similarity   99.0%;  Pred. No. 9e-101;
  Matches  191;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 8
AAW61392
ID   AAW61392 standard; protein; 193 AA.
XX
AC   AAW61392;
XX
DT   02-OCT-1998  (first entry)
XX
DE   Human bcl-y protein.
XX
KW   bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
XX
OS   Homo sapiens.
XX
PN   US5789201-A.
XX
PD   04-AUG-1998.
XX
PF   11-FEB-1997;   97US-00798897.
XX
PR   23-FEB-1996;   96US-0012201P.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1998-446079/38.
DR   N-PSDB; AAV28334.
XX
PT   Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
PT   recombinant protein for use in treating uncontrolled cell growth e.g.
PT   cancers.
XX
PS   Example; Column 17/18; 27pp; English.
XX
CC   The mammalian bcl-y protein is a member of the bcl-2 family, components
CC   in the cell death pathway. The bcl-2 family have both apoptotic activity
CC   and the apoptosis blocking activity. bcl-y falls in the apoptosis
CC   activity category. The recombinant protein may be used to prevent
CC   uncontrolled cell growth, either by its direct administration to
CC   recombinant genetic constructs to increase its expression in vivo. Also,
CC   antisense constructs can be used in disorders where prevention of cell
CC   death is desired
XX
SQ   Sequence 193 AA;

  Query Match             98.6%;  Score 995;  DB 2;  Length 193;
  Best Local Similarity   98.4%;  Pred. No. 3.2e-100;
  Matches  190;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              ||||||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193


RESULT 9
AAW97392
ID   AAW97392 standard; protein; 193 AA.
XX
AC   AAW97392;
XX
DT   20-MAY-1999  (first entry)
XX
DE   The human bcl-y protein.
XX
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
OS   Homo sapiens.
XX
PN   US5883229-A.
XX
PD   16-MAR-1999.
XX
PF   25-NOV-1997;   97US-00978523.
XX
PR   23-FEB-1996;   96US-0012201P.
PR   11-FEB-1997;   97US-00798897.
```

XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1999-214150/18.
DR N-PSDB; AAX15946.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT modulating programmed cell death.
XX
PS Claim 1; Col 17-18; 26pp; English.
XX
CC The present sequence represents human bcl-y protein (Hbcl-y). The
CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-
CC y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC - conditions where cells under go premature cell death as a result of
CC triggers which may or may not be apparent. They may also be used in this
CC way to develop cell lines which remain viable in culture for an extended
CC period. In contrast, if they act as cell death stimulators, Rbcl-y and
CC Hbcl-y may be used to treat conditions associated with prolonged cell
CC life span such as cancer (especially kaposi's sarcoma and lung cancer)
CC and auto/hyperimmune diseases. They may also be used to cause cell death
CC in, and hence control, parasites
XX
SQ Sequence 193 AA;

Query Match 98.6%; Score 995; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 3.2e-100;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193
```

RESULT 10
AAW36047
ID AAW36047 standard; protein; 193 AA.
XX
AC AAW36047;
XX
DT 22-APR-1998 (first entry)
XX
DE Human bcl-w protein.
XX
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease.
XX
OS Homo sapiens.
XX
PN WO9735971-A1.
XX
PD 02-OCT-1997.
XX
PF 27-MAR-1997; 97WO-AU000199.
XX
PR 27-MAR-1996; 96AU-00008965.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Cory S, Adams JM, Gibson LM, Holmgreen SP;
XX
DR WPI; 1997-489635/45.
DR N-PSDB; AAT96577.
XX
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
PT inhibit cell survival, e.g. for treatment of cancer and degenerative
PT diseases.
XX
PS Claim 6; Page 48; 86pp; English.
XX
CC This sequence represents a novel human protein, bcl-w, encoded by the bcl
CC -2 gene family and extracted from an adult brain library. This gene
CC promotes cell survival, so its modulation is useful in treatment of
CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
CC ischaemia, human immunodeficiency virus infection or in cell transplants.
CC Up-regulation of the gene can also be used to modify cell lines cultured
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
CC and to increase survival of primary explants during genetic modification.
CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
CC antibody production or screening of potential modulators
XX
SQ Sequence 193 AA;

Query Match 98.4%; Score 993; DB 2; Length 193;
Best Local Similarity 97.9%; Pred. No. 5.3e-100;
Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193
```

RESULT 11
AAY05532
ID AAY05532 standard; protein; 193 AA.
XX
AC AAY05532;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human Bcl-w protein essential for spermatogenesis.
XX
KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW animal model.
XX
OS Homo sapiens.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.

XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
DR WPI; 1999-243890/20.
DR N-PSDB; AAX25134.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w.
XX
PS Disclosure; Page 37; 52pp; English.
XX
CC The present sequence is described of a derivative of human Bcl-w (see
CC also AAY05530), a pro-survival member of the Bcl-2 family that is widely
CC expressed and which is essential for spermatogenesis. The invention
CC relates generally to a method of treatment and to an animal model for the
CC identification of molecules and genetic sequences useful for inducing or
CC reducing fertility of male animals. Methods are provided for the
CC treatment of infertility, or for reducing fertility, by modulating
CC spermatogenesis. An animal model carries a mutation is at least one
CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
CC associated with bcl-w. Such animals have disorganised seminferous tubules
CC and are substantially infertile, but possess no other major abnormalities
CC as determined by histological examination. They can be used to screen for
CC therapeutic molecules including genetic sequences capable of inducing,
CC enhancing or otherwise facilitating spermatogenesis in animals, or which
CC can induce infertility
XX
SQ Sequence 193 AA;

Query Match 98.4%; Score 993; DB 2; Length 193;
Best Local Similarity 97.9%; Pred. No. 5.3e-100;
Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              |||||:|||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||:|||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        181 GALVTVGAFFASK 193
```

RESULT 12
AAW97394
ID AAW97394 standard; protein; 192 AA.
XX
AC AAW97394;
XX
DT 20-MAY-1999 (first entry)
XX
DE Mammalian bcl-y protein.
XX
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
OS Mammalia.
XX
PN US5883229-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-00978523.
XX
PR 23-FEB-1996; 96US-0012201P.
PR 11-FEB-1997; 97US-00798897.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1999-214150/18.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT modulating programmed cell death.
XX
PS Claim 2; Col 19-22; 26pp; English.
XX
CC The present sequence represents a mammalian bcy-1 protein. The
CC specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
CC thought to be involved in programmed cell death (apoptosis and necrosis).
CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
CC with a disruption of the cell death pathway. If they act as cell death
CC inhibitors, they may be used in therapies to treat subjects suffering
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC degenerative diseases (especially multiple sclerosis), myocardial
CC infarction, vitally induced cell death, aging, spinal cord injuries and
CC amyotrophic lateral sclerosis- conditions where cells under go premature
CC cell death as a result of triggers which may or may not be apparent. They
CC may also be used in this way to develop cell lines which remain viable in
CC culture for an extended period. In contrast, if they act as cell death
CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated
CC with prolonged cell life span such as cancer (especially kaposi's sarcoma
CC and lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites
XX
SQ Sequence 192 AA;

Query Match 98.1%; Score 990; DB 2; Length 192;
Best Local Similarity 98.4%; Pred. No. 1.1e-99;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
              ||||| ||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60

Qy         62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120

Qy        122 VQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
              ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

Qy        182 ALVTVGAFFASK 193
              ||||||||||||
Db        181 ALVTVGAFFASK 192
```

RESULT 13
AAY05533
ID AAY05533 standard; protein; 192 AA.
XX
AC AAY05533;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse Bcl-w protein deritvative.
XX

KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW animal model.
XX
OS Mus sp.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
DR WPI; 1999-243890/20.
DR N-PSDB; AAX25135.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w.
XX
PS Disclosure; Page 39; 52pp; English.
XX
CC The present sequence is described of a derivative of mouse Bcl-w (see
CC also AAY05531), a pro-survival member of the Bcl-2 family that is widely
CC expressed and which is essential for spermatogenesis. The derivative
CC lacks the 24 N-terminal amino acids of Bcl-w. The invention relates
CC generally to a method of treatment and to an animal model for the
CC identification of molecules and genetic sequences useful for inducing or
CC reducing fertility of male animals. Methods are provided for the
CC treatment of infertility, or for reducing fertility, by modulating
CC spermatogenesis. An animal model carries a mutation is at least one
CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
CC associated with bcl-w. Such animals have disorganised seminferous tubules
CC and are substantially infertile, but possess no other major abnormalities
CC as determined by histological examination. They can be used to screen for
CC therapeutic molecules including genetic sequences capable of inducing,
CC enhancing or otherwise facilitating spermatogenesis in animals, or which
CC can induce infertility
XX
SQ Sequence 192 AA;

```
  Query Match             95.9%;  Score 967.5;  DB 2;  Length 192;
  Best Local Similarity   95.9%;  Pred. No. 3.2e-97;
  Matches  185;  Conservative    5;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              | ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db          1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
              |||||:|||||||||||||||:||||||||||:|||||||||| | ||:||||||
Db        121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179

Qy        181 GALVTVGAFFASK 193
              |||||||||||||
Db        180 GALVTVGAFFASK 192
```

RESULT 14
ADP88350
ID ADP88350 standard; protein; 183 AA.
XX
AC ADP88350;
XX
DT 09-SEP-2004 (first entry)
XX
DE Derivative of human Bcl-w protein.
XX
KW Bcl-w; human; protein structure; protein co-ordinate data; mutant;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 128
FT /note= "wild-type Ala substituted by Glu"
XX
PN WO2004050697-A1.
XX
PD 17-JUN-2004.
XX
PF 03-DEC-2003; 2003WO-AU001624.
XX
PR 03-DEC-2002; 2002AU-00953259.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Hinds MG, Huang DCS, Day CL;
XX
DR WPI; 2004-487529/46.
XX
PT Solution useful for identifying or selecting agents that are capable of
PT inhibiting biological activity of Bcl-w, comprises molecule that has Bcl-
PT w active site defined by specific structure coordinates of Bcl-w amino
PT acid residues.
XX
PS Claim 16; Page 805-806; 810pp; English.
XX
CC The present invention relates to a solution comprising a molecule or
CC molecular complex that comprises at least a fragment of Bcl-w. Also
CC disclosed is the structure of Bcl-w, in the form of protein coordinate
CC data. The solution is useful for identifying, selecting or designing
CC agents that are capable of inhibiting or potentiating one or more
CC biological activity of Bcl-w, and in solving the structures of other
CC proteins with similar structure. It is also useful for characterizing the
CC three-dimensional structure of the Bcl-w molecule, molecular complex or
CC its derivative. The present sequence is a derivative of the human Bcl-w
CC protein.
XX
SQ Sequence 183 AA;

```
  Query Match             93.9%;  Score 947;  DB 8;  Length 183;
  Best Local Similarity   98.4%;  Pred. No. 5.3e-95;
  Matches  180;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

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RESULT 15
AAW36048
ID AAW36048 standard; protein; 168 AA.
XX
AC AAW36048;
XX

DT 22-APR-1998 (first entry)
XX
DE Mouse bcl-w protein.
XX
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease.
XX
OS Mus sp.
XX
PN WO9735971-A1.
XX
PD 02-OCT-1997.
XX
PF 27-MAR-1997; 97WO-AU000199.
XX
PR 27-MAR-1996; 96AU-00008965.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Cory S, Adams JM, Gibson LM, Holmgreen SP;
XX
DR WPI; 1997-489635/45.
DR N-PSDB; AAT96578.
XX
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
PT inhibit cell survival, e.g. for treatment of cancer and degenerative
PT diseases.
XX
PS Claim 6; Page 50-51; 86pp; English.
XX
CC This sequence represents a novel protein, bcl-w, encoded by the mouse bcl
CC -2 gene family. This gene promotes cell survival, so its modulation is
CC useful in treatment of cancer or auto-immune diseases, degenerative
CC diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular
CC degeneration, hypoxia, ischaemia, human immunodeficiency virus infection
CC or in cell transplants. Up-regulation of the gene can also be used to
CC modify cell lines cultured in vivo, e.g. to develop new lines, to
CC facilitate isolation of hybridomas and to increase survival of primary
CC explants during genetic modification. It can be used to produce
CC recombinant Bcl-w for therapy, diagnosis, antibody production or
CC screening of potential modulators
XX
SQ Sequence 168 AA;

Query Match 86.8%; Score 876; DB 2; Length 168;
Best Local Similarity 97.0%; Pred. No. 2.8e-87;
Matches 163; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWA 168
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Search completed: April 10, 2005, 22:40:50
Job time : 66 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 10, 2005, 22:43:04 ; Search time 227.5 Seconds
(without alignments)
281.650 Million cell updates/sec

Title: US-09-925-674B-9
Perfect score: 1009
Sequence: 1 MATPASTPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1006	99.7	193	9	US-09-925-674A-9	Sequence 9, Appli
2	1000	99.1	193	9	US-09-925-674A-7	Sequence 7, Appli
3	1000	99.1	193	16	US-10-450-366-6	Sequence 6, Appli
4	759	75.2	365	10	US-09-809-391-696	Sequence 696, App
5	759	75.2	365	10	US-09-882-171-696	Sequence 696, App
6	759	75.2	365	15	US-10-164-861-696	Sequence 696, App
7	631.5	62.6	228	16	US-10-659-705-2	Sequence 2, Appli
8	457.5	45.3	179	15	US-10-402-017-6	Sequence 6, Appli
9	448.5	44.4	199	15	US-10-402-017-8	Sequence 8, Appli
10	441.5	43.8	219	15	US-10-402-017-10	Sequence 10, Appl
11	436.5	43.3	219	15	US-10-402-017-12	Sequence 12, Appl
12	432.5	42.9	229	16	US-10-659-705-7	Sequence 7, Appli
13	432.5	42.9	411	16	US-10-792-517-2	Sequence 2, Appli
14	429.5	42.6	233	15	US-10-402-017-4	Sequence 4, Appli
15	427.5	42.4	233	9	US-09-734-846-2	Sequence 2, Appli
16	427.5	42.4	233	9	US-09-952-278-6	Sequence 6, Appli
17	427.5	42.4	233	14	US-10-101-482-14	Sequence 14, Appl
18	427.5	42.4	233	14	US-10-072-830-4	Sequence 4, Appli
19	427.5	42.4	233	14	US-10-169-223-10	Sequence 10, Appl
20	427.5	42.4	233	14	US-10-302-262-2	Sequence 2, Appli
21	427.5	42.4	233	15	US-10-116-275-171	Sequence 171, App
22	427.5	42.4	233	16	US-10-450-366-5	Sequence 5, Appli
23	427.5	42.4	233	16	US-10-659-705-8	Sequence 8, Appli
24	415.5	41.2	239	15	US-10-148-953A-3	Sequence 3, Appli
25	414.5	41.1	152	14	US-10-158-769-2	Sequence 2, Appli
26	414.5	41.1	233	16	US-10-659-705-3	Sequence 3, Appli
27	412	40.8	236	13	US-10-087-192-1953	Sequence 1953, Ap
28	411.5	40.8	239	14	US-10-277-693A-10	Sequence 10, Appl
29	411.5	40.8	239	15	US-10-003-632C-10	Sequence 10, Appl
30	411.5	40.8	239	15	US-10-003-632C-13	Sequence 13, Appl
31	409.5	40.6	239	8	US-08-726-211-5	Sequence 5, Appli
32	409.5	40.6	239	10	US-09-993-420A-8	Sequence 8, Appli
33	409.5	40.6	239	14	US-10-101-482-12	Sequence 12, Appl
34	409.5	40.6	239	14	US-10-072-830-2	Sequence 2, Appli
35	409.5	40.6	239	14	US-10-141-618-12	Sequence 12, Appl
36	409.5	40.6	239	14	US-10-053-645A-21	Sequence 21, Appl
37	409.5	40.6	239	15	US-10-387-961A-5	Sequence 5, Appli
38	409.5	40.6	239	15	US-10-003-632C-1	Sequence 1, Appli
39	409.5	40.6	239	15	US-10-003-632C-3	Sequence 3, Appli
40	409.5	40.6	239	15	US-10-148-953A-1	Sequence 1, Appli
41	409.5	40.6	239	15	US-10-148-953A-2	Sequence 2, Appli
42	409.5	40.6	239	15	US-10-297-321-2	Sequence 2, Appli
43	409.5	40.6	239	16	US-10-450-366-4	Sequence 4, Appli
44	409.5	40.6	239	16	US-10-770-668-16	Sequence 16, Appl
45	409.5	40.6	485	16	US-10-792-517-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-925-674A-9
; Sequence 9, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mouse
US-09-925-674A-9

Query Match 99.7%; Score 1006; DB 9; Length 193;
Best Local Similarity 99.5%; Pred. No. 1.2e-96;
Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
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Qy        181 GALVTVGAFFASK 193
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Db        181 GALVTVGAFFASK 193

RESULT 2
US-09-925-674A-7
; Sequence 7, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
;  APPLICANT: AMRAD Operations Pty Ltd
;  TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
;  TITLE OF INVENTION:  FAMILY OF APOPTOSIS-CONTROLLING GENES
;  FILE REFERENCE: 11686a
;  CURRENT APPLICATION NUMBER: US/09/925,674A
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/925,674
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: PN8965
;  PRIOR FILING DATE: 1996-03-27
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: HUMAN
US-09-925-674A-7

  Query Match             99.1%;  Score 1000;  DB 9;  Length 193;
  Best Local Similarity   99.0%;  Pred. No. 5.2e-96;
  Matches  191;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

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              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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Qy        181 GALVTVGAFFASK 193
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Db        181 GALVTVGAFFASK 193

RESULT 3
US-10-450-366-6
; Sequence 6, Application US/10450366
; Publication No. US20040115667A1
; GENERAL INFORMATION:
;  APPLICANT: Tschopp, Jorg
;  APPLICANT:  Hoffmann, Kay
;  TITLE OF INVENTION: DNA-Sequences, Which Code For An Apoptosis Signal Transduction Pr
;  FILE REFERENCE: 11436*3
;  CURRENT APPLICATION NUMBER: US/10/450,366
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: PCT/EP01/14597
;  PRIOR FILING DATE: 2001-12-12
;  PRIOR APPLICATION NUMBER: DE 100 61 766.2
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: DE 101 00 280.7
;  PRIOR FILING DATE: 2001-01-04
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human Bcl-W
US-10-450-366-6

  Query Match             99.1%;  Score 1000;  DB 16;  Length 193;
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Qy        121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
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Db        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy        181 GALVTVGAFFASK 193
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Db        181 GALVTVGAFFASK 193

RESULT 4
US-09-809-391-696
; Sequence 696, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P2
;  CURRENT APPLICATION NUMBER: US/09/809,391
;  CURRENT FILING DATE:  2001-03-16
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 761
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 696
;   LENGTH: 365
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-809-391-696

  Query Match             75.2%;  Score 759;  DB 10;  Length 365;
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RESULT 5
US-09-882-171-696
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; Publication No. US20030175858A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P2
;  CURRENT APPLICATION NUMBER: US/09/882,171
;  CURRENT FILING DATE:  2001-06-18
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; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
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; PRIOR APPLICATION NUMBER: 60/056,872
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; PRIOR APPLICATION NUMBER: 60/056,882
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; PRIOR APPLICATION NUMBER: 60/056,888
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; PRIOR APPLICATION NUMBER: 60/056,880
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,894
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,911
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,636
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,874
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,910
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,864
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,631
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,892
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/047,595
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,588
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,585
; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,590
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match 75.2%; Score 759; DB 10; Length 365;
Best Local Similarity 98.6%; Pred. No. 1.7e-70;
Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGW 144
              |||:||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGW 144
```

RESULT 6
US-10-164-861-696
; Sequence 696, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 696
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-861-696

Query Match 75.2%; Score 759; DB 15; Length 365;
Best Local Similarity 98.6%; Pred. No. 1.7e-70;
Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy        121 QVQDWMVAYLETRLADWIHSSGGW 144
              |||:||||||||||||||||||||
Db        121 QVQEWMVAYLETRLADWIHSSGGW 144
```

RESULT 7
US-10-659-705-2
; Sequence 2, Application US/10659705
; Publication No. US20040117867A1
; GENERAL INFORMATION:
; APPLICANT: Look, A. Thomas
; APPLICANT: Langenau, David M.
; TITLE OF INVENTION: Transgenic Cancer Models in Fish
; FILE REFERENCE: 112706.123
; CURRENT APPLICATION NUMBER: US/10/659,705
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 60/409,585
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BCL2 proteins
US-10-659-705-2

Query Match 62.6%; Score 631.5; DB 16; Length 228;
Best Local Similarity 67.4%; Pred. No. 1.9e-57;
Matches 124; Conservative 20; Mismatches 37; Indels 3; Gaps 1;

```
Qy         10 TRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLH 69
              :|||| | | ||| |:  |       | |:  || |||||||||| | |: ||::: |:|
Db         48 SRALVEDLVRYKLCQRSLV---PEPSGAASCALHSAMRAAGDEFEERPRQAFSEISTQIH 104

Qy         70 VTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAY 129
              ||||:|  || :|:  ||||| |||||||||||||||||| ||: ::|||||  |
Db        105 VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY 164

Qy        130 LETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAF 189
              ||| |  || |:|||  |  ||||||:||||| |||||||::|||||||||||:||||
Db        165 LETNLDRWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL 224

Qy        190 FASK 193
              ||||
Db        225 FASK 228
```

```
RESULT 8
US-10-402-017-6
; Sequence 6, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
;  APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
;  TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
;  TITLE OF INVENTION:  such cells
;  FILE REFERENCE: Case 1/1314
;  CURRENT APPLICATION NUMBER: US/10/402,017
;  CURRENT FILING DATE:  2003-03-28
;  PRIOR APPLICATION NUMBER: US 60/369,307
;  PRIOR APPLICATION NUMBER: April 2, 2002
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 179
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del26-83)
US-10-402-017-6

  Query Match             45.3%;  Score 457.5;  DB 15;  Length 179;
  Best Local Similarity   52.0%;  Pred. No. 2e-39;
  Matches   91;  Conservative   21;  Mismatches   56;  Indels    7;  Gaps    2;

Qy         11 RALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHV 70
              |:|| ||: ||| |||| |      ||  : ||:| |||||| |:|| |||| :|||:
Db          6 RELVVDFLSYKLSQKGYSWSAA-----AAAAVKQALREAGDEFELRYRRAFSDLTSQLHI 60

Qy         71 TPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYL 130
              |||:| | | || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||
Db         61 TPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYL 120

Qy        131 ETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                 |  ||  :|||  |  |||: |  |:|: :|    |      : | | ||:|
Db        121 NDHLEPWIQDNGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 175


RESULT 9
US-10-402-017-8
; Sequence 8, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
;  APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
;  TITLE OF INVENTION: Host cells having improved survival properties and methods to gen
;  TITLE OF INVENTION:  such cells
;  FILE REFERENCE: Case 1/1314
;  CURRENT APPLICATION NUMBER: US/10/402,017
;  CURRENT FILING DATE:  2003-03-28
;  PRIOR APPLICATION NUMBER: US 60/369,307
;  PRIOR APPLICATION NUMBER: April 2, 2002
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 199
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del46-83)
US-10-402-017-8

  Query Match             44.4%;  Score 448.5;  DB 15;  Length 199;
  Best Local Similarity   47.9%;  Pred. No. 2e-38;
  Matches   91;  Conservative   21;  Mismatches   61;  Indels   17;  Gaps    2;

Qy         11 RALVADFVGYKLRQKGYVC---------------GAGPGEGPAADPLHQAMRAAGDEFET 55
              | || ||: ||| ||||                 |       ||  : ||:| ||||||
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESERAAAAAAVKQALREAGDEFEL 65

Qy         56 RFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEM 115
                 |:|| |||| :|||:|||:| | | || :|||: | ||||:|||| || ||| |||:|||
Db         66 RYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEM 125

Qy        116 EPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--GNWASVRTV 173
                 : || ::  ||  ||   |  ||  :||| |  |||: |  |:|: :|    |
Db        126 QVLVSRIASWMATYLNDHLEPWIQDNGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMT 185

Qy        174 LTGAVALGAL 183
                 : | | ||:|
Db        186 VAGVVLLGSL 195


RESULT 10
US-10-402-017-10
; Sequence 10, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
;  APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
;  TITLE OF INVENTION: Host cells having improved survival properties and methods to gene
;  TITLE OF INVENTION:  such cells
;  FILE REFERENCE: Case 1/1314
;  CURRENT APPLICATION NUMBER: US/10/402,017
;  CURRENT FILING DATE:  2003-03-28
;  PRIOR APPLICATION NUMBER: US 60/369,307
;  PRIOR APPLICATION NUMBER: April 2, 2002
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 219
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del66-83)
US-10-402-017-10

  Query Match             43.8%;  Score 441.5;  DB 15;  Length 219;
  Best Local Similarity   43.3%;  Pred. No. 1.2e-37;
  Matches   91;  Conservative   21;  Mismatches   61;  Indels   37;  Gaps    2;

Qy         11 RALVADFVGYKLRQKGYV----------------------------------CGAGPGE 35
              | || ||: ||| ||||                                  |
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESERETPSAINGNPSWHLADSPAV 65

Qy         36 GPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGR 95
                 ||  : ||:| |||||| |:|| |||| :|||:|||:| | | || :|||: | ||||
Db         66 AAAAAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGR 125

Qy         96 LVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGA 155
              :|||| || ||| |||:|||: || ::  ||  ||   |  ||  :|||  |  |||: |
Db        126 IVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQDNGGWDTFVELYGNNA 185

Qy        156 LEEARRLRE--GNWASVRTVLTGAVALGAL 183
                 |:|: :|    |      : | | ||:|
Db        186 AAESRKGQERFNRWFLTGMTVAGVVLLGSL 215


RESULT 11
US-10-402-017-12
; Sequence 12, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
;  APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
;  TITLE OF INVENTION: Host cells having improved survival properties and methods to gene
;  TITLE OF INVENTION:  such cells
;  FILE REFERENCE: Case 1/1314
;  CURRENT APPLICATION NUMBER: US/10/402,017
;  CURRENT FILING DATE:  2003-03-28
;  PRIOR APPLICATION NUMBER: US 60/369,307
;  PRIOR APPLICATION NUMBER: April 2, 2002
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 219
```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del26-83)
US-10-402-017-12

Query Match 43.3%; Score 436.5; DB 15; Length 219;
Best Local Similarity 44.1%; Pred. No. 4.1e-37;
Matches 93; Conservative 22; Mismatches 57; Indels 39; Gaps 4;

```
Qy          11 RALVADFVGYKLRQKGY----------------------------VCGAGPGEGPAAD-- 40
               |  ||  ||: ||| ||||                            | |||  |   : |
Db           6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESERAAAAAVNGA-TGHSSSLDAR 64

Qy          41 ------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWG 94
                     : ||:| |||||| |:|| |||| :|||:|||:| | | || :|||: | |||
Db          65 EVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWG 124

Qy          95 RLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDG 154
               |:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :|||  |  |||:
Db         125 RIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQDNGGWDTFVELYGNN 184

Qy         155 ALEEARRLRE--GNWASVRTVLTGAVALGAL 183
               |  |:|: :|    |      : | | ||:|
Db         185 AAAESRKGQERFNRWFLTGMTVAGVVLLGSL 215
```

RESULT 12
US-10-659-705-7
; Sequence 7, Application US/10659705
; Publication No. US20040117867A1
; GENERAL INFORMATION:
; APPLICANT: Look, A. Thomas
; APPLICANT: Langenau, David M.
; TITLE OF INVENTION: Transgenic Cancer Models in Fish
; FILE REFERENCE: 112706.123
; CURRENT APPLICATION NUMBER: US/10/659,705
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 60/409,585
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BCL2 proteins
US-10-659-705-7

Query Match 42.9%; Score 432.5; DB 16; Length 229;
Best Local Similarity 41.7%; Pred. No. 1.1e-36;
Matches 95; Conservative 22; Mismatches 62; Indels 49; Gaps 4;

```
Qy          11 RALVADFVGYKLRQKGY----------------------VCGAGPGEGP---------- 37
               |  ||  |||  |||  |:|:                   |    |   |
Db           6 RELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65

Qy          38 ------------AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                           |  : ||:| |||||| |:|| |||| :|||:|||:| | | || :|
Db          66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE 125

Qy          86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWA 145
               ||  | ||||:|||| || ||| |||:|||  |||::  ||  ||    |  ||  :|||
Db         126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWE 185

Qy         146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
               |  |||:  |   |  ||:|     : :||||   | |: :|:  : |
Db         186 RFVDLYGNNA---AAELRKGQETFNKWLLTGATVAGVLL-LGSLLSRK 229
```

RESULT 13
US-10-792-517-2
; Sequence 2, Application US/10792517
; Publication No. US20040152179A1
; GENERAL INFORMATION:
; APPLICANT: Youle et al.
; TITLE OF INVENTION: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL
; TITLE OF INVENTION: FUSION PROTEIN INHIBITS APOPTOSIS
; FILE REFERENCE: 4239-55417
; CURRENT APPLICATION NUMBER: US/10/792,517
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/639,245
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/149,220
; PRIOR FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: genetic fusion
US-10-792-517-2

Query Match 42.9%; Score 432.5; DB 16; Length 411;
Best Local Similarity 39.9%; Pred. No. 2.4e-36;
Matches 93; Conservative 26; Mismatches 63; Indels 51; Gaps 4;

```
Qy          11 RALVADFVGYKLRQKGY--------------------------VCGAGP----GEGPAA 39
               |  ||  ||: ||| ||||                        |     : ||
Db          26 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 85

Qy          40 D-----------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                :                 : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db          86 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 145

Qy          82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
               | :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   | ||  :
Db         146 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQEN 205

Qy         142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGALVTVGAFFAS 192
               |||  |  |||: |  |:|: :|    |       : | | ||:| :  |: |:
Db         206 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRKAYSAA 258
```

RESULT 14
US-10-402-017-4
; Sequence 4, Application US/10402017
; Publication No. US20030219871A1
; GENERAL INFORMATION:
; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER
; TITLE OF INVENTION: Host cells having improved survival properties and methods to gene
; TITLE OF INVENTION: such cells
; FILE REFERENCE: Case 1/1314
; CURRENT APPLICATION NUMBER: US/10/402,017
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/369,307
; PRIOR APPLICATION NUMBER: April 2, 2002
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Cricetulus griseus
US-10-402-017-4

Query Match 42.6%; Score 429.5; DB 15; Length 233;
Best Local Similarity 41.3%; Pred. No. 2.4e-36;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

```
Qy          11 RALVADFVGYKLRQKGY-----------------------------------------V 28
               |  ||  ||: ||| ||||                                       |
Db           6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESERETPSAINGNPSWHLADSPAV 65
```

```
Qy          29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
               ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db          66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy          81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
               || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db         125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQD 184

Qy         141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
               :|||. |  |||: |  |:|: :|    |       : | | ||:|
Db         185 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT 15
US-09-734-846-2
; Sequence 2, Application US/09734846
; Patent No. US20010007025A1
; GENERAL INFORMATION:
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Dean, Nicholas M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Nickoloff, Brian J.
;  APPLICANT:  Zhang, QingQing
;  TITLE OF INVENTION:  Antisense Modulation of bcl-x Expression
;  FILE REFERENCE:  ISPH-0528
;  CURRENT APPLICATION NUMBER: US/09/734,846
;  CURRENT FILING DATE:  2000-12-12
;  PRIOR APPLICATION NUMBER:      09/277,020
;  PRIOR FILING DATE:      1998-03-26
;  PRIOR APPLICATION NUMBER:      09/167,921
;  PRIOR FILING DATE:      1998-10-07
;  PRIOR APPLICATION NUMBER:  09/323,743
;  PRIOR FILING DATE:  1999-06-02
;  NUMBER OF SEQ ID NOS:  74
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-734-846-2

  Query Match             42.4%;  Score 427.5;  DB 9;  Length 233;
  Best Local Similarity   40.6%;  Pred. No. 3.8e-36;
  Matches   91;  Conservative   23;  Mismatches   59;  Indels   51;  Gaps    4;

Qy          11 RALVADFVGYKLRQKGY--------------------------VCGAGP----GEGPAA 39
               | || ||: ||| ||||                          |     : ||
Db           6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy          40 D------------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
               :                  : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db          66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125

Qy          82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
               | :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :
Db         126 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQEN 185

Qy         142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
               |||  |  |||: |  |:|: :|    |       : | | ||:|
Db         186 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


Search completed: April 10, 2005, 22:59:28
Job time : 228.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 10, 2005, 22:09:08 ; Search time 17 Seconds
(without alignments)
1092.343 Million cell updates/sec

Title: US-09-925-674B-9
Perfect score: 1009
Sequence: 1 MATPASTPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	428.5	42.5	233	2	I49056	bcl-x long - mouse
2	427.5	42.4	233	2	B47537	apoptosis regulato
3	424.5	42.1	233	2	S51761	BCL-X protein - ra
4	423.5	42.0	233	2	A37332	transforming prote
5	414	41.0	232	2	S24390	transforming prote
6	411.5	40.8	239	1	TVHUA1	transforming prote
7	411	40.7	236	2	I67432	BCL-2 - rat (fragm
8	406	40.2	236	2	I53744	gene bcl-2 protein
9	405	40.1	236	1	TVMSA1	transforming prote
10	404.5	40.1	233	2	I67431	BCL-X-Long - rat
11	402	39.8	236	2	JC7383	B-cell lymphoma 2
12	378	37.5	190	2	A47537	apoptosis regulato
13	377.5	37.4	214	2	I49057	bcl-x transmembran
14	374.5	37.1	227	2	JE0203	apoptosis regulato
15	356	35.3	216	2	B37332	transforming prote
16	348.5	34.5	199	1	TVMSB1	transforming prote
17	345	34.2	205	1	TVHUB1	transforming prote
18	277.5	27.5	154	2	I58194	gene bcl-2 protein
19	182	18.0	170	2	I49055	bcl-x short - mous
20	174	17.2	176	2	I67435	gene bcl-xshort pr
21	171	16.9	211	2	S58873	Bak protein - huma
22	168	16.7	211	2	S58875	cdn-2 protein - hu
23	158.5	15.7	192	2	D47538	bcl-2-associated p
24	154	15.3	192	2	A47538	bcl-2-associated p
25	151	15.0	261	2	H88578	protein ced-9 [imp
26	151	15.0	280	2	A53189	apoptosis suppress
27	150.5	14.9	133	2	I53295	bcl-2-associated p
28	147.5	14.6	179	2	JC7255	Bax-delta protein
29	147.5	14.6	218	2	B47538	bcl-2-associated p
30	142	14.1	177	2	S54778	NR-13 protein - qu
31	138.5	13.7	143	2	I38921	bcl-2-associated p
32	138	13.7	255	2	JC7567	Mcl-1a protein - z
33	116	11.5	175	2	I39055	Bcl-2 related - hu
34	116	11.5	350	2	A47476	BCL2 homolog MCL1
35	105	10.4	172	2	I49449	hemopoietic-specif
36	88	8.7	185	2	B83217	hypothetical prote
37	87	8.6	3433	1	GNWVKV	genome polyprotein
38	86.5	8.6	301	2	T36534	probable lipase/es
39	86	8.5	270	2	AI2598	dihydrodipicolinat
40	86	8.5	279	2	B97381	dihydrodipicolinat
41	84.5	8.4	358	1	AJLCQB	glutamate-ammonia
42	83.5	8.3	872	2	H95160	alanyl-tRNA synthe
43	83.5	8.3	872	2	G98026	alanine-tRNA ligas
44	83	8.2	3430	1	GNWVWV	genome polyprotein
45	81.5	8.1	886	2	A32758	beta-amyloid-like

ALIGNMENTS

RESULT 1
I49056
bcl-x long - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49056; S52866
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A;Reference number: I49055; MUID:95052604; PMID:7963517
A;Accession: I49056
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 <RES>
A;Cross-references: UNIPROT:Q64373; EMBL:U10101; NID:g506647; PIDN:AAA82173.1; PID:g5066
R;Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
submitted to the EMBL Data Library, November 1994
A;Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line throug
A;Reference number: S52866
A;Accession: S52866
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-233 <KAM>
A;Cross-references: EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PID:g695623
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.5%; Score 428.5; DB 2; Length 233;
Best Local Similarity 41.3%; Pred. No. 1.8e-32;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

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Qy         11 RALVADFVGYKLRQKGY----------------------------------------V 28
                | || ||: ||| ||||                                        |
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy         29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db         66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy         81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
               || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db        125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy        141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
               :|||  |  |||: |  |:|: :|    |      : | | ||:|
Db        185 NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
```

RESULT 2
B47537
apoptosis regulator bcl-xL - human
N;Alternate names: bcl-2-related protein
N;Contains: apoptosis regulator bcl-xS

```
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: B47537; C47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A;Reference number: A47537; MUID:93364977; PMID:8358789
A;Accession: B47537
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 <BOI>
A;Cross-references: UNIPROT:Q07817; GB:L20121; NID:g510900; PIDN:CAA80661.1; PID:g510901
A;Accession: C47537
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-69,'G',71-125,189-233 <BO2>
A;Cross-references: GB:L20122; NID:g623236; PIDN:CAA80662.1; PID:g623237
C;Genetics:
A;Gene: GDB:BCL2L
A;Cross-references: GDB:228079
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; apoptosis
F;1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>
F;1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <MA2>

  Query Match             42.4%;  Score 427.5;  DB 2;  Length 233;
  Best Local Similarity   40.6%;  Pred. No. 2.2e-32;
  Matches   91;  Conservative   23;  Mismatches   59;  Indels   51;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGY-------------------------VCGAGP----GEGPAA 39
                | || ||: ||| ||||                         |     : ||
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy         40 D------------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
              :                  : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db         66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125

Qy         82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
              | :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :
Db        126 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQEN 185

Qy        142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
              |||   |  |||: |  |:|: :|     |       : | | ||:|
Db        186 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT 3
S51761
BCL-X protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51761; S51762
R;Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994
A;Reference number: S51761
A;Accession: S51761
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <MIC>
A;Cross-references: UNIPROT:P53563; EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g6071
A;Experimental source: embryonic; brain
A;Accession: S51762
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125,189-233 <MI2>
A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PID:g607178
A;Experimental source: embryonic; brain
A;Note: smaller form due to splicing
C;Genetics:
A;Introns: 125/3
C;Superfamily: bcl apoptosis regulator, inhibitory type

  Query Match             42.1%;  Score 424.5;  DB 2;  Length 233;
  Best Local Similarity   41.3%;  Pred. No. 4.1e-32;
  Matches   92;  Conservative   22;  Mismatches   56;  Indels   53;  Gaps    4;

Qy         13 LVADFVGYKLRQKGY-----------------------------------------VCG 30
              || ||: ||| ||||                                         | |
Db          8 LVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAVNG 67

Qy         31 AGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQV 82
              |  |   : |          : ||:| |||||| |:|| |||| :|||:|||:| | | ||
Db         68 A-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQV 126

Qy         83 SDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSG 142
              :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :|
Db        127 VNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENG 186

Qy        143 GWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
              ||  |  |||: |  |:|: :|     |       : | | ||:|
Db        187 GWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT 4
A37332
transforming protein (bcl-2-alpha) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A37332; S35453
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: A37332
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-233 <EGU>
A;Cross-references: UNIPROT:Q00709; EMBL:D11381
C;Genetics:
A;Introns: 189/3
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: mitochondrion; transforming protein; transmembrane protein

  Query Match             42.0%;  Score 423.5;  DB 2;  Length 233;
  Best Local Similarity   38.0%;  Pred. No. 5.1e-32;
  Matches   87;  Conservative   32;  Mismatches   61;  Indels   49;  Gaps    4;

Qy          9 DTRALVADFVGYKLRQKGYVCGAG-------PGEGPAADP------------------- 41
              | | :|  :: ||| |:||   ||       |   ||| |
Db         10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69

Qy         42 -----------------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSD 84
                              :| |:| ||||| |:: |: :: |||:|| :|  ||  | :
Db         70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129

Qy         85 ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGW 144
              |||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   | :||  :|||
Db        130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW 189

Qy        145 AEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
              |  |||:       | | : :| |::|:|:  | :|| :|:||:   |
Db        190 DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 233


RESULT 5
S24390
transforming protein (Bcl-2) homolog - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S24390
R;Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
Biochim. Biophys. Acta 1132, 109-113, 1992
A;Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue c
A;Reference number: S24390; MUID:92379084; PMID:1511008
A;Accession: S24390
A;Status: preliminary
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A;Molecule type: mRNA
A;Residues: 1-232 <CAZ>
A;Cross-references: UNIPROT:Q00709; EMBL:Z11961; NID:g62969; PIDN:CAA78018.1; PID:g62970
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: mitochondrion; transmembrane protein

Query Match 41.0%; Score 414; DB 2; Length 232;
Best Local Similarity 37.7%; Pred. No. 3.9e-31;
Matches 86; Conservative 32; Mismatches 62; Indels 48; Gaps 4;

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Qy          9 DTRALVADFVGYKLRQKGYVCGAG-------PGEGPAADP------------------- 41
              | | :|  :: ||| |:||   ||       |   ||| |
Db         10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPSPPARL 69

Qy         42 ----------------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                            :| |:| |||||  |::| |: :: |||:|| :|  ||  | :|
Db         70 LLVRCPRLRGCAAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTATGRFVAVVEE 129

Qy         86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWA 145
              ||: | || |:|||| ||  :| ||||:|| |||  :  ||  ||   | :||  :|||
Db        130 LFRDGVNWVRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGWD 189

Qy        146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
              |  |||:      | | : :| |::|:|:  | :|| :|:|||:   |
Db        190 AFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 232
```

RESULT 6
TVHUA1
transforming protein bcl-2, splice form alpha - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: C37332; A29409; S02452; A24428; A27622; B27622
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: C37332
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-239 <EGU>
A;Cross-references: UNIPROT:P10415
A;Note: this report is a correction
R;Tsujimoto, Y.; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A;Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene
A;Reference number: A29409; MUID:86259760; PMID:3523487
A;Accession: A29409
A;Molecule type: mRNA
A;Residues: 1-95,'A',97-109,'G',111-236,'S',238-239 <TSU>
A;Cross-references: GB:M13994; NID:g179366; PIDN:AAA51813.1; PID:g179367
A;Note: this sequence has been corrected in reference A37332
R;Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeye
EMBO J. 7, 123-131, 1988
A;Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2
A;Reference number: S02452; MUID:88196071; PMID:2834197
A;Accession: S02452
A;Molecule type: mRNA
A;Residues: 1-239 <SET>
R;Cleary, M.L.; Smith, S.D.; Sklar, J.
Cell 47, 19-28, 1986
A;Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglo
A;Reference number: A24428; MUID:87002488; PMID:2875799
A;Accession: A24428
A;Molecule type: mRNA
A;Residues: 1-58,'T',60-116,'R',118-239 <CLE>
A;Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
R;Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhshi, A.
Oncogene Res. 2, 263-275, 1988
A;Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:
A;Reference number: A27622; MUID:88217344; PMID:3285301
A;Accession: A27622
A;Molecule type: mRNA
A;Residues: 1-58,'T',60-239 <HUA>
A;Accession: B27622
A;Molecule type: DNA
A;Residues: 1-6,'S',8-58,'T',60-128,'C',130-239 <HUA2>
A;Note: the sequence was determined from the germline gene
C;Comment: Constitutive expression of BCL2 following t(14:18) chromosomal translocation
C;Genetics:
A;Gene: GDB:BCL2
A;Cross-references: GDB:119031; OMIM:151430
A;Map position: 18q21.3-18q21.3
C;Function:
A;Description: blocks apoptosis in hematopoietic cells
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 40.8%; Score 411.5; DB 1; Length 239;
Best Local Similarity 37.0%; Pred. No. 7e-31;
Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;

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Qy          9 DTRALVADFVGYKLRQKGYVCGAG-------------------PGE-------------- 35
              | | :|  :: ||| |:||   ||                   ||
Db         10 DNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAPGIFSSQPGHTPHPAASRDPVART 69

Qy         36 -------------GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR 78
                          |||  |    :|  :| |||:|  |:|| |:::::|||:|| :|: |
Db         70 SPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR 129

Qy         79 FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWI 138
              |  | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||
Db        130 FATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWI 189

Qy        139 HSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
               :|||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db        190 QDNGGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
```

RESULT 7
I67432
BCL-2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I67432
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equine
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A;Reference number: I53295; MUID:95129487; PMID:7828536
A;Accession: I67432
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-236 <RES>
A;Cross-references: UNIPROT:P49950; EMBL:U34964; NID:g1004378; PIDN:AAA77687.1; PID:g1004
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.7%; Score 411; DB 2; Length 236;
Best Local Similarity 36.2%; Pred. No. 7.6e-31;
Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

```
Qy          9 DTRALVADFVGYKLRQKGY--------------------------------------- 27
              | | :|  :: ||| |:||
Db         10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRRAPTPGIFSFQPESNRTPAVHRDTAART 69

Qy         28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                   |  |||   |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db         70 SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy         82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
              | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db        130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMYPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy        142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
               |||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db        190 GGWDAFVELYG----PSMRPLFDFSWQSLKTLLSLAL-VGACITLGAYLGHK 236
```

```
RESULT 8
I53744
gene bcl-2 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I53744
R;Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
Gene 140, 291-292, 1994
A;Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.
A;Reference number: I53744; MUID:94193015; PMID:8144041
A;Accession: I53744
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-236 <RES>
A;Cross-references: UNIPROT:P49950; GB:L14680; NID:g408946; PIDN:AAA53662.1; PID:g408947
C;Genetics:
A;Gene: bcl-2
C;Superfamily: bcl apoptosis regulator, inhibitory type

  Query Match             40.2%;  Score 406;  DB 2;  Length 236;
  Best Local Similarity   35.8%;  Pred. No. 2.2e-30;
  Matches   83;  Conservative   34;  Mismatches   63;  Indels   52;  Gaps    3;

Qy          9 DTRALVADFVGYKLRQKGY----------------------------------------- 27
              | | :|  :: ||| |:||
Db         10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART 69

Qy         28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                    |  |||    |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db         70 SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy         82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
              | :|||: | ||||:|||| ||  :|  |||:|| ||||  :  ||  ||   |  ||  :
Db        130 VVEELFRDGVNWGRIVAFFEFGGVMCVGSVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy        142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
              |||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db        190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236


RESULT 9
TVMSA1
transforming protein bcl-2-alpha - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 28-Jul-2003
C;Accession: A25960; E37332
R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
A;Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homol
A;Reference number: A90893; MUID:87187643; PMID:3032455
A;Accession: A25960
A;Molecule type: DNA
A;Residues: 1-236 <NEG>
A;Cross-references: GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1; PID:g387109
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: E37332
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-33,'E',34-220,'AL',223-236 <EGU>
C;Genetics:
A;Gene: BCL2
A;Introns: 192/3
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane prc

  Query Match             40.1%;  Score 405;  DB 1;  Length 236;
  Best Local Similarity   37.1%;  Pred. No. 2.8e-30;
  Matches   86;  Conservative   33;  Mismatches   61;  Indels   52;  Gaps    5;

Qy          9 DTRALVADFVGYKLRQKGYVCGAG-----------PG---------------------- 34
              | | :|  :: ||| |:||   ||             ||
Db         10 DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHREMAART 69

Qy         35 ---------EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                      |||  |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db         70 SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy         82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
              | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db        130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy        142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
              |||  |  |||       | | : :| |::|:|:    :|| :|:||:   |
Db        190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLS-LPWVGACITLGAYLGHK 236


RESULT 10
I67431
BCL-X-Long - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I67431
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equine
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A;Reference number: I53295; MUID:95129487; PMID:7828536
A;Accession: I67431
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 <RES>
A;Cross-references: UNIPROT:P53563; EMBL:U34963; NID:g1004376; PIDN:AAA77686.1; PID:g100
C;Superfamily: bcl apoptosis regulator, inhibitory type

  Query Match             40.1%;  Score 404.5;  DB 2;  Length 233;
  Best Local Similarity   39.6%;  Pred. No. 3e-30;
  Matches   89;  Conservative   22;  Mismatches   61;  Indels   53;  Gaps    4;

Qy         11 RALVADFVGYKLRQKGY-----------------------------------------V 28
              | || ||: ||| ||||                                         |
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV 65

Qy         29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
              ||  |   : |          : ||:| |||||| |:|| |||| :|||:|||:  | |
Db         66 NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFE 124

Qy         81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
              || :|||: | ||||:||   || ||| |||:|||: || ::  ||  ||   |  ||
Db        125 QVVNELFRDGVNWGRIVASSSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy        141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
              :|||  |  |||:    |:|: :|    |       : | | ||:|
Db        185 NGGWDTFVDLYGNNTAPESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT 11
JC7383
B-cell lymphoma 2 protein - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7383
R;Tomicic, M.T.; Christmann, M.; Kaina, B.
Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A;Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A;Reference number: JC7383
A;Contents: Ovary
A;Accession: JC7383
A;Molecule type: mRNA
A;Residues: 1-236 <TOM>
A;Cross-references: UNIPROT:Q9JJV8; GB:AJ271720
C;Comment: This protein has anti-apoptotic function, and supports cell survival.
```

```
C;Genetics:
A;Gene: bcl-2
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: B-cell lymphoma; ovary

  Query Match             39.8%;  Score 402;  DB 2;  Length 236;
  Best Local Similarity   35.3%;  Pred. No. 5.3e-30;
  Matches   82;  Conservative   34;  Mismatches   64;  Indels   52;  Gaps    3;

Qy          9 DTRALVADFVGYKLRQKGY---------------------------------------- 27
              | | :|  :: ||| |:||
Db         10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART 69

Qy         28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                    |   ||   |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db         70 SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy         82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
              | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db        130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy        142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
              |||  |  |||       | | : :| |::|:|: |: :|| :|:|  :   |
Db        190 GGWDAFVELYG----PSVRPLFDFSWLSLKTLLSLAL-VGACITLGTYLGHK 236


RESULT 12
A47537
apoptosis regulator bcl-x - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A;Reference number: A47537; MUID:93364977; PMID:8358789
A;Accession: A47537
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-190 <BOI>
A;Cross-references: UNIPROT:Q07816; GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1;
C;Superfamily: bcl apoptosis regulator, inhibitory type

  Query Match             37.5%;  Score 378;  DB 2;  Length 190;
  Best Local Similarity   43.8%;  Pred. No. 7e-28;
  Matches   81;  Conservative   14;  Mismatches   44;  Indels   46;  Gaps    3;

Qy         11 RALVADFVGYKLRQKGY----------------------VCGAGPGEGP---------- 37
              | ||  ||| ||| |:|:                      |   |   |
Db          6 RELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65

Qy         38 ------------AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                         |  : ||:| |||||| |:|| |||| :|||:|||:| | | || :|
Db         66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE 125

Qy         86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWA 145
              ||  | ||||:|||| || ||| |||:|||  |||::  ||  ||   |  ||  :|||
Db        126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWV 185

Qy        146 EFTAL 150
                |||
Db        186 R-TAL 189


RESULT 13
I49057
bcl-x transmembrane deleted - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49057
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A;Reference number: I49055; MUID:95052604; PMID:7963517
A;Accession: I49057
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-214 <RES>
A;Cross-references: UNIPROT:Q64373; EMBL:U10102; NID:g506649; PIDN:AAA82174.1; PID:g5066
C;Genetics:
A;Gene: bcl-x-long
C;Superfamily: bcl apoptosis regulator, inhibitory type

  Query Match             37.4%;  Score 377.5;  DB 2;  Length 214;
  Best Local Similarity   42.8%;  Pred. No. 9e-28;
  Matches   80;  Conservative   16;  Mismatches   40;  Indels   51;  Gaps    3;

Qy         11 RALVADFVGYKLRQKGY-----------------------------------------V 28
              | || ||: ||| ||||                                         |
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy         29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
              ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db         66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy         81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
              || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db        125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy        141 SGGWAEF 147
              :|||  |
Db        185 NGGWDTF 191


RESULT 14
JE0203
apoptosis regulator bcl-x isoform - human
N;Alternate names: h-bcl-xbeta
C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE0203
R;Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.
Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A;Title: Identification of a human cDNA encoding a novel bcl-x isoform.
A;Reference number: JE0203; MUID:98340865; PMID:9675101
A;Accession: JE0203
A;Molecule type: mRNA
A;Residues: 1-227 <BAN>
A;Cross-references: UNIPROT:Q07817; GB:U72398; NID:g1622940; PIDN:AAB17354.1; PID:g16229
C;Genetics:
A;Gene: bcl-x
A;Map position: 20
C;Superfamily: bcl apoptosis regulator, inhibitory type

  Query Match             37.1%;  Score 374.5;  DB 2;  Length 227;
  Best Local Similarity   40.8%;  Pred. No. 1.8e-27;
  Matches   82;  Conservative   18;  Mismatches   50;  Indels   51;  Gaps    3;

Qy         11 RALVADFVGYKLRQKGY-----------------------------------------V 28
              | || ||: ||| ||||                                         |
Db          6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy         29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
              ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db         66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy         81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
              || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db        125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE 184

Qy        141 SGGWAEFTALYGDGALEEARR 161
              :|||     |   :|  :|
Db        185 NGGWVRTKPLVCPFSLASGQR 205


RESULT 15
```

B37332
transforming protein (bcl-2-beta) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003
C;Accession: B37332; S35452
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: B37332
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-216 <EGU>
A;Cross-references: EMBL:D11381; EMBL:D11382
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 35.3%; Score 356; DB 2; Length 216;
Best Local Similarity 38.4%; Pred. No. 9.1e-26;
Matches 71; Conservative 21; Mismatches 49; Indels 44; Gaps 2;

```
Qy          9 DTRALVADFVGYKLRQKGYVCGAG-------PGEGPAADP------------------- 41
              | | :|  :: ||| |:||   ||       |   ||| |
Db         10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69

Qy         42 -----------------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSD 84
                              :| |:| |||||  |::| |: :: |||:|| :|  ||  | :
Db         70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129

Qy         85 ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGW 144
              |||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   | :||  :|||
Db        130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW 189

Qy        145 AEFTA 149
                |
Db        190 VRACA 194
```

Search completed: April 10, 2005, 22:44:41
Job time : 17 secs